



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 122834

To: Patricia Patten (Leith)
Location: REM-3C04&3C3D11
Art Unit: 1654
Wednesday, May 26, 2004

Case Serial Number: 09/830964

From: Beverly Shears
Location: Remsen Bldg.
RM 1A54
Phone: 571-272-2528

beverly.shears@uspto.gov

Search Notes

122834

STIC-Biotech/ChemLib

From: STIC-ILL
Sent: Monday, May 24, 2004 3:47 PM
To: STIC-Biotech/ChemLib
Subject: FW: 09/830,964

CITE

See below.

-----Original Message-----

From: Leith, Patricia
Sent: Monday, May 24, 2004 3:21 PM
To: STIC-ILL
Subject: 09/830,964

Please search SEQ ID NO. 1 of 09/830,964.

Thank you.

Patty Leith

US Patent and Trademark Office
Tech Center 1600
Biotechnology
Art Unit 1654
REM 3C04

(571) 272-0968

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M protein - protein search, using sw model
un on: May 25, 2004, 11:21:39 ; Search time 184 Seconds
(without alignments)
875.265 Million cell updates/sec

title: US-09-830-964-1
effect score: 846
equences: 1 APPRLICDSRLVRYLEAK.....SNFLRGLKLYTGBACRTGD 165

coring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 6019581 seqs, 976053577 residues

total number of hits satisfying chosen parameters: 6019581

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_AA_Main:*

- 1: /cgn2_6/prodata/2/paa/PCTUS COMB.pcp.*
- 2: /cgn2_6/prodata/2/paa/US06 COMB.pcp.*
- 3: /cgn2_6/prodata/2/paa/US07 COMB.pcp.*
- 4: /cgn2_6/prodata/2/paa/US08 COMB.pcp.*
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- 6: /cgn2_6/prodata/2/paa/US082 COMB.pcp.*
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- 8: /cgn2_6/prodata/2/paa/US084 COMB.pcp.*
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- 30: /cgn2_6/prodata/2/paa/US104 COMB.pcp.*
- 31: /cgn2_6/prodata/2/paa/US106 COMB.pcp.*
- 32: /cgn2_6/prodata/2/paa/US107 COMB.pcp.*
- 33: /cgn2_6/prodata/2/paa/US60 COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

1	846	100.0	165	1	PCT-US03-31974-73	Sequence 73, Appl
2	846	100.0	165	1	PCT-US99-26238-1	Sequence 1, Appli
3	846	100.0	165	1	PCT-US99-26240-1	Sequence 1, Appli
4	846	100.0	165	1	PCT-US99-26241-1	Sequence 1, Appli
5	846	100.0	165	18	US-09-426-566-1	Sequence 1, Appli
6	846	100.0	165	20	US-09-687-981-1	Sequence 1, Appli
7	846	100.0	165	23	US-09-830-964-1	Sequence 1, Appli
8	846	100.0	165	23	US-09-830-967-1	Sequence 1, Appli
9	846	100.0	165	23	US-09-830-968-1	Sequence 1, Appli
10	846	100.0	165	23	US-09-853-731-1	Sequence 1, Appli
11	846	100.0	165	23	US-09-854-018-1	Sequence 1, Appli
12	846	100.0	165	24	US-09-945-517-1	Sequence 1, Appli
13	846	100.0	165	26	US-10-014-363-1	Sequence 1, Appli
14	846	100.0	165	28	US-10-241-356-1	Sequence 1, Appli
15	846	100.0	165	28	US-10-293-551-1	Sequence 73, Appl
16	846	100.0	165	30	US-10-410-897-73	Sequence 73, Appl
17	846	100.0	165	30	US-10-410-913-73	Sequence 73, Appl
18	846	100.0	165	30	US-10-410-930-73	Sequence 73, Appl
19	846	100.0	165	30	US-10-410-945-73	Sequence 73, Appl
20	846	100.0	165	30	US-10-410-962-73	Sequence 73, Appl
21	846	100.0	165	30	US-10-410-980-73	Sequence 73, Appl
22	846	100.0	165	30	US-10-410-997-73	Sequence 73, Appl
23	846	100.0	165	30	US-10-411-012-73	Sequence 73, Appl
24	846	100.0	165	30	US-10-411-026-73	Sequence 73, Appl
25	846	100.0	165	30	US-10-411-037-73	Sequence 73, Appl
26	846	100.0	165	30	US-10-411-043-73	Sequence 73, Appl
27	846	100.0	165	30	US-10-411-044-73	Sequence 73, Appl
28	846	100.0	165	30	US-10-411-049-73	Sequence 73, Appl
29	846	100.0	165	32	US-10-706-701-1	Sequence 1, Appli
30	846	100.0	166	1	PCT-US98-14497-2	Sequence 2, Appli
31	846	100.0	166	3	US-07-766-964A-3	Sequence 3, Appli
32	846	100.0	166	4	US-08-049-802-37	Sequence 37, Appl
33	846	100.0	166	6	US-08-223-263-7	Sequence 7, Appli
34	846	100.0	166	6	US-08-223-263A-7	Sequence 7, Appli
35	846	100.0	166	6	US-08-232-533-37	Sequence 37, Appl
36	846	100.0	166	6	US-08-249-376-7	Sequence 7, Appli
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40	846	100.0	166	8	US-08-422-020-7	Sequence 7, Appli
41	846	100.0	166	8	US-08-422-020A-7	Sequence 7, Appli
42	846	100.0	166	8	US-08-422-194-7	Sequence 7, Appli
43	846	100.0	166	8	US-08-422-194A-7	Sequence 7, Appli
44	846	100.0	166	8	US-08-422-548-7	Sequence 7, Appli
45	846	100.0	166	8	US-08-422-727-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
PCT-US03-31974-73
; Sequence 73, Application PC/TUS0331974
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryne
; TITLE OF INVENTION: ERYTHROPOIETIN
; FILE REFERENCE: 040853-01-5083WO
; CURRENT APPLICATION NUMBER: PCT/US03/31974
; CURRENT FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: PCT/US02/32263
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 10/287,994
; PRIOR FILING DATE: 2002-11-5
; PRIOR APPLICATION NUMBER: US 10/360,770
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US 10/369,779

REMODELING AND GLYCOCONGUATION OF

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; PRIOR FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US 10/410,945
; PRIOR FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-31974-73

Query Match      100.0%; Score 846; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.7e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 APPRLICDSRVLYRLLEAKAEENITTCAGHCSLNENITVPDTKVNIFYAKRMEVGQQA 60

QY 61 VEVWQGLALLSEAVLRGOALLVNSSQWPEPLQHLVDKAVSGLSRLTLLRALGAKKEAIS 120
Db 61 VEVWQGLALLSEAVLRGOALLVNSSQWPEPLQHLVDKAVSGLSRLTLLRALGAKKEAIS 120

QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGD 165
Db 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGD 165

RESULT 2
PCT-US99-26238-1
; Sequence 1, Application PC/TUS99926238
; GENERAL INFORMATION:
; APPLICANT: Sterrenbeld Biotechnologie North America, Inc.
; APPLICANT: Carcagno, Carlos Miguel
; APPLICANT: Criscuolo, Marcelo
; APPLICANT: Melo, Carlos
; APPLICANT: Vidal, Juan Alejandro
; TITLE OF INVENTION: Host Cells Expressing Recombinant Human Erythropoietin
; FILE REFERENCE: 1792.002PC02
; CURRENT FILING DATE: 1999-11-08
; EARLIER FILING DATE: 1999-02-23
; EARLIER APPLICATION NUMBER: AR 99-01-00679
; EARLIER FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-26238-1

Query Match      100.0%; Score 846; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.7e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 APPRLICDSRVLYRLLEAKAEENITTCAGHCSLNENITVPDTKVNIFYAKRMEVGQQA 60

QY 61 VEVWQGLALLSEAVLRGOALLVNSSQWPEPLQHLVDKAVSGLSRLTLLRALGAKKEAIS 120
Db 61 VEVWQGLALLSEAVLRGOALLVNSSQWPEPLQHLVDKAVSGLSRLTLLRALGAKKEAIS 120

QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGD 165
Db 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGD 165

RESULT 3
PCT-US99-26240-1
; Sequence 1, Application PC/TUS99926240
; GENERAL INFORMATION:
; APPLICANT: Sterrenbeld Biotechnologie North America, Inc.
; APPLICANT: Carcagno, Carlos Miguel
; APPLICANT: Criscuolo, Marcelo
; APPLICANT: Melo, Carlos
; APPLICANT: Vidal, Juan Alejandro
; TITLE OF INVENTION: Method for the Massive Culture of Cells Producing Recombinant Human Erythropoietin
; FILE REFERENCE: 1792.004PC02
; CURRENT FILING DATE: 1999-11-08
; EARLIER FILING DATE: 1999-02-23
; EARLIER APPLICATION NUMBER: AR 99-01-00681
; EARLIER FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-26240-1

Query Match      100.0%; Score 846; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.7e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 VEVWQGLALLSEAVLRGOALLVNSSQWPEPLQHLVDKAVSGLSRLTLLRALGAKKEAIS 120
Db 61 VEVWQGLALLSEAVLRGOALLVNSSQWPEPLQHLVDKAVSGLSRLTLLRALGAKKEAIS 120

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Db 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGD 165

RESULT 4
PCT-US99-26241-1
; Sequence 1, Application PC/TUS99926241
; GENERAL INFORMATION:
; APPLICANT: Sterrenbeld Biotechnologie North America, Inc.
; APPLICANT: Carcagno, Carlos Miguel
; APPLICANT: Criscuolo, Marcelo
; APPLICANT: Melo, Carlos
; APPLICANT: Vidal, Juan Alejandro
; TITLE OF INVENTION: Methods of Purifying Recombinant Human Erythropoietin from Cell
; FILE REFERENCE: 1792.003PC02
; CURRENT FILING DATE: 1999-11-08
; EARLIER FILING DATE: 1999-02-23
; EARLIER APPLICATION NUMBER: AR 99-01-00680
; EARLIER FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-26241-1

Query Match      100.0%; Score 846; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.7e-89;
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Db 1 APPRLICDSRVLYRLLEAKAEENITTCAGHCSLNENITVPDTKVNIFYAKRMEVGQQA 60

QY 61 VEVWQGLALLSEAVLRGOALLVNSSQWPEPLQHLVDKAVSGLSRLTLLRALGAKKEAIS 120
Db 61 VEVWQGLALLSEAVLRGOALLVNSSQWPEPLQHLVDKAVSGLSRLTLLRALGAKKEAIS 120

QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGD 165
Db 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGD 165
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b 61 VEVWQGLALLSEAVLRGQALLVNSSQWPEPLQHLVDKAVSGLSRLTTLRALGAQKEAIS 120
Y 121 PPDAASAAPLRTITADTFRKLFRVYSNFIPLRGKLYTGACRTGD 165
b 121 PPDAASAAPLRTITADTFRKLFRVYSNFIPLRGKLYTGACRTGD 165

RESULT 5

S-09-426-566-1
Sequence 1, Application US/09426566
GENERAL INFORMATION:
APPLICANT: Burke, Paul
APPLICANT: Klumb, Lisa
APPLICANT: Murphy, Keith
APPLICANT: Herberger, John
APPLICANT: French, Donna
TITLE OF INVENTION: BIODEGRADABLE MICROPARTICLES FOR THE SUSTAINED DELIVERY
TITLE OF INVENTION: OF NOVEL ERYTHROPOIETIN STIMULATING PROTEIN
FILE REFERENCE: A-626
CURRENT APPLICATION NUMBER: US/09/426,566
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 165
TYPE: PRT
ORGANISM: HUMAN
US-09-426-566-1

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Best Local Similarity 100.0%; Pred. No. 1.7e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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b 61 VEVWQGLALLSEAVLRGQALLVNSSQWPEPLQHLVDKAVSGLSRLTTLRALGAQKEAIS 120
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b 121 PPDAASAAPLRTITADTFRKLFRVYSNFIPLRGKLYTGACRTGD 165

RESULT 6

US-09-687-981-1
Sequence 1, Application US/09687981
GENERAL INFORMATION:
APPLICANT: Burke, Paul
APPLICANT: Klumb, Lisa
APPLICANT: Murphy, Keith
APPLICANT: Herberger, John
APPLICANT: French, Donna
TITLE OF INVENTION: BIODEGRADABLE MICROPARTICLES FOR THE SUSTAINED DELIVERY OF NOVEL
TITLE OF INVENTION: ERYTHROPOIETIN STIMULATING PROTEIN
FILE REFERENCE: A-626A
CURRENT APPLICATION NUMBER: US/09/687,981
CURRENT FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 09/426,566
PRIOR FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 165
TYPE: PRT
ORGANISM: Homo sapiens
US-09-687-981-1

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Best Local Similarity 100.0%; Pred. No. 1.7e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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b 1 APPLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVFYAWKRMVEVGQA 60
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b 61 VEVWQGLALLSEAVLRGQALLVNSSQWPEPLQHLVDKAVSGLSRLTTLRALGAQKEAIS 120
Y 121 PPDAASAAPLRTITADTFRKLFRVYSNFIPLRGKLYTGACRTGD 165
b 121 PPDAASAAPLRTITADTFRKLFRVYSNFIPLRGKLYTGACRTGD 165

RESULT 7

US-09-830-964-1
Sequence 1, Application US/09830964
GENERAL INFORMATION:
APPLICANT: Sterrenbeld Biotechnologie North America, Inc.
APPLICANT: Carcagno, Carlos Miguel
APPLICANT: Criscuolo, Marcelo
APPLICANT: Melo, Carlos
APPLICANT: Vidal, Juan Alejandro
TITLE OF INVENTION: Methods of Purifying Recombinant Human
TITLE OF INVENTION: Erythropoietin from Cell Culture Supernatants
FILE REFERENCE: 1909.0030002
CURRENT APPLICATION NUMBER: US/09/830,964
CURRENT FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: AR 99-01-00680
PRIOR FILING DATE: 1999-02-23
PRIOR APPLICATION NUMBER: AR 98-01-05610
PRIOR FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 165
TYPE: PRT
ORGANISM: Homo sapiens
US-09-830-964-1

Query Match 100.0%; Score 846; DB 23; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.7e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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b 1 APPLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVFYAWKRMVEVGQA 60
Y 61 VEVWQGLALLSEAVLRGQALLVNSSQWPEPLQHLVDKAVSGLSRLTTLRALGAQKEAIS 120
b 61 VEVWQGLALLSEAVLRGQALLVNSSQWPEPLQHLVDKAVSGLSRLTTLRALGAQKEAIS 120
Y 121 PPDAASAAPLRTITADTFRKLFRVYSNFIPLRGKLYTGACRTGD 165
b 121 PPDAASAAPLRTITADTFRKLFRVYSNFIPLRGKLYTGACRTGD 165

RESULT 8

US-09-830-967-1
Sequence 1, Application US/09830967
GENERAL INFORMATION:
APPLICANT: Sterrenbeld Biotechnologie North America, Inc.
APPLICANT: Carcagno, Carlos Miguel
APPLICANT: Criscuolo, Marcelo
APPLICANT: Melo, Carlos
APPLICANT: Vidal, Juan Alejandro
TITLE OF INVENTION: Host Cells Expressing Recombinant Human Erythropoietin
FILE REFERENCE: 1909.0020002
CURRENT APPLICATION NUMBER: US/09/830,967
CURRENT FILING DATE: 1999-11-08

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; PRIOR APPLICATION NUMBER: AR 99-01-00679
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: AR 98-01-05609
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-830-967-1

Query Match      100.0%; Score 846; DB 23; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.7e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
QY 121 PDAAASAPLRTITADTFKLFVYSNFRGKLYTGEACRTGD 165
DB 121 PDAAASAPLRTITADTFKLFVYSNFRGKLYTGEACRTGD 165
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RESULT 9
US-09-830-968-1
; Sequence 1, Application US/09830968
; GENERAL INFORMATION:
; APPLICANT: Sterrenbeld Biotechnologie North America, Inc.
; APPLICANT: Carcagno, Carlos Miguel
; APPLICANT: Criscuolo, Marcelo
; APPLICANT: Melo, Carlos
; APPLICANT: Vidal, Juan Alejandro
; TITLE OF INVENTION: Method for the Massive Culture of Cells
; TITLE OF INVENTION: Producing Recombinant Human Erythropoietin
; FILE REFERENCE: 1909.0040002
; CURRENT APPLICATION NUMBER: US/09/830,968
; CURRENT FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: AR 99-01-00681
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: AR 98-01-05611
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-830-968-1
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Query Match      100.0%; Score 846; DB 23; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.7e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
QY 121 PDAAASAPLRTITADTFKLFVYSNFRGKLYTGEACRTGD 165
DB 121 PDAAASAPLRTITADTFKLFVYSNFRGKLYTGEACRTGD 165
```

RESULT 10

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US-09-853-731-1
; Sequence 1, Application US/09853731
; GENERAL INFORMATION:
; APPLICANT: Papadimitriou, Apollon
; TITLE OF INVENTION: Erythropoietin Composition
; FILE REFERENCE: 20619 US
; CURRENT APPLICATION NUMBER: US/09/853,731
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP/00110355.5
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-731-1

Query Match      100.0%; Score 846; DB 23; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.7e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
DB 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
QY 121 PDAAASAPLRTITADTFKLFVYSNFRGKLYTGEACRTGD 165
DB 121 PDAAASAPLRTITADTFKLFVYSNFRGKLYTGEACRTGD 165
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RESULT 11
US-09-854-018-1
; Sequence 1, Application US/09854018
; GENERAL INFORMATION:
; APPLICANT: Herberger, John
; TITLE OF INVENTION: Secondary Drying of Microparticles Using Pressurized Carbon Dioxide
; FILE REFERENCE: A-786
; CURRENT APPLICATION NUMBER: US/09/854,018
; CURRENT FILING DATE: 2001-05-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Human
US-09-854-018-1
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Query Match      100.0%; Score 846; DB 23; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.7e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
DB 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
QY 121 PDAAASAPLRTITADTFKLFVYSNFRGKLYTGEACRTGD 165
DB 121 PDAAASAPLRTITADTFKLFVYSNFRGKLYTGEACRTGD 165
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RESULT 12
US-09-945-517-1
; Sequence 1, Application US/09945517
; GENERAL INFORMATION:
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APPLICANT: Li, Tiansheng
APPLICANT: Chang, Byeong
APPLICANT: Sloey, Christopher
TITLE OF INVENTION: L-METHIONINE AS A STABILIZER FOR NESP/EPO IN HSA-FREE FORMULATION
FILE REFERENCE: A-803
CURRENT APPLICATION NUMBER: US/09/945,517
CURRENT FILING DATE: 2001-08-30
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patent in version 3.0
SEQ ID NO 1
LENGTH: 165
TYPE: PRT
ORGANISM: Homo sapiens
US-09-945-517-1

Query Match 100.0%; Score 846; DB 24; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.7e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
DB 1 APPRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120
QY 121 PPDAASAPLRTITADTFKRLFRVYSNFRGKLYTGEACRTGD 165
DB 121 PPDAASAPLRTITADTFKRLFRVYSNFRGKLYTGEACRTGD 165

RESULT 13
US-10-014-363-1
; Sequence 1, Application US/10014363
; GENERAL INFORMATION:
; APPLICANT: Burs, Josef
; APPLICANT: Engel, Alfred
; APPLICANT: Franze, Reinhard
; APPLICANT: Hilger, Bernd
; APPLICANT: Schurig, Hartmut Ernst
; APPLICANT: Fischer, Wilhelm
; APPLICANT: Wozny, Manfred
; TITLE OF INVENTION: Erythropoietin Conjugates
; FILE REFERENCE: Case 20805
; CURRENT APPLICATION NUMBER: US/10/014,363
; CURRENT FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-363-1

Query Match 100.0%; Score 846; DB 26; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.7e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
DB 1 APPRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120
QY 121 PPDAASAPLRTITADTFKRLFRVYSNFRGKLYTGEACRTGD 165
DB 121 PPDAASAPLRTITADTFKRLFRVYSNFRGKLYTGEACRTGD 165

US-10-241-356-1
; Sequence 1, Application US/10241356
; GENERAL INFORMATION:
; APPLICANT: Tischer, Wilhelm
; TITLE OF INVENTION: DIGLYCOSYLATED ERYTHROPOIETIN
; FILE REFERENCE: 20971
; CURRENT APPLICATION NUMBER: US/10/241,356
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: EP 01122555.4
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-241-356-1

Query Match 100.0%; Score 846; DB 28; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.7e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
DB 1 APPRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120
QY 121 PPDAASAPLRTITADTFKRLFRVYSNFRGKLYTGEACRTGD 165
DB 121 PPDAASAPLRTITADTFKRLFRVYSNFRGKLYTGEACRTGD 165

RESULT 15
US-10-293-551-1
; Sequence 1, Application US/10293551
; GENERAL INFORMATION:
; APPLICANT: Bailon, Pascal
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1097 nonprovisional
; CURRENT APPLICATION NUMBER: US/10/293,551
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US/09/604,938
; PRIOR FILING DATE: 2000-06-27
; PRIOR FILING DATE: 1999-11-17
; PRIOR FILING DATE: 1999-08-13
; PRIOR FILING DATE: 1999-08-13
; PRIOR FILING DATE: 1999-08-23
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-551-1

Query Match 100.0%; Score 846; DB 28; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.7e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
DB 1 APPRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120

QY 121 PPDAASAAPLETTITADTFERKLFVYSNPLRGKUKLYTGEACRTGD 165
DB 121 PPDAASAAPLETTITADTFERKLFVYSNPLRGKUKLYTGEACRTGD 165

Search completed: May 25, 2004, 11:27:23
Job time : 185 secs

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WM protein - protein search, using sw model

Run on: May 25, 2004, 11:22:10 ; Search time 20 Seconds
(without alignments)
312.305 Million cell updates/sec

Title: US-09-830-964-1
Perfect score: 846
Sequence: 1 APRLLCDNSVRLRYLLEAK.....SNFLRGKLYTGEACRTGD 165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 254384 seqs, 37855110 residues

Total number of hits satisfying chosen parameters: 254384

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New:

- 1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	846	100.0	165	1	PCT-US04-11494-73
2	846	100.0	165	6	US-10-634-477-1
3	846	100.0	165	6	US-10-780-297-1
4	846	100.0	166	6	US-10-780-297-2
5	846	100.0	166	6	US-10-658-834A-201
6	846	100.0	166	6	US-10-773-939-2
7	846	100.0	166	6	US-10-774-149-2
8	846	100.0	192	6	US-10-775-204-593
9	846	100.0	192	6	US-10-775-204-594
10	846	100.0	192	6	US-10-775-204-603
11	846	100.0	192	6	US-10-775-204-1689
12	846	100.0	192	6	US-10-775-204-1690
13	846	100.0	192	6	US-10-775-204-1691
14	846	100.0	192	6	US-10-775-204-1828
15	846	100.0	192	6	US-10-775-204-1829
16	846	100.0	192	6	US-10-775-204-1830
17	846	100.0	193	1	PCT-US04-10353-3
18	846	100.0	193	1	PCT-US04-10353-9
19	846	100.0	193	1	PCT-US04-13099-10
20	846	100.0	193	1	PCT-US04-13099-22
21	846	100.0	193	1	PCT-US04-13099-112
22	846	100.0	435	6	US-10-761-593A-22
23	846	100.0	436	6	US-10-761-593A-18
24	846	100.0	437	6	US-10-761-593A-20
25	846	100.0	768	6	US-10-775-204-1521
26	846	100.0	768	6	US-10-775-204-1522

RESULT 1
PCT-US04-11494-73
; Sequence 73, Application PC/TUS0411494
; GENERAL INFORMATION:
; APPLICANT: Neosec Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Cayne
; TITLE OF INVENTION: GLYCOPREGYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; FILE REFERENCE: 040853-01-5051WO
; CURRENT APPLICATION NUMBER: PCT/US04/11494
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/334,233
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/334,301
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: PCT/US02/32263
; PRIOR FILING DATE: 2002-10-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-11494-73

ALIGNMENTS

Sequence 1523, Ap
Sequence 1660, Ap
Sequence 1661, Ap
Sequence 1662, Ap
Sequence 387, App
Sequence 367, App
Sequence 371, App
Sequence 374, App
Sequence 375, App
Sequence 377, App
Sequence 378, App
Sequence 404, App
Sequence 409, App
Sequence 401, App
Sequence 959, App
Sequence 967, App
Sequence 952, App
Sequence 955, App
Sequence 958, App

27 846 100.0 768 6 US-10-775-204-1523
28 846 100.0 768 6 US-10-775-204-1660
29 846 100.0 768 6 US-10-775-204-1661
30 846 100.0 768 6 US-10-775-204-1662
31 846 100.0 769 6 US-10-775-204-387
32 846 100.0 777 6 US-10-775-204-367
33 846 100.0 777 6 US-10-775-204-371
34 846 100.0 777 6 US-10-775-204-374
35 846 100.0 777 6 US-10-775-204-375
36 846 100.0 777 6 US-10-775-204-377
37 846 100.0 777 6 US-10-775-204-378
38 846 100.0 951 6 US-10-775-204-404
39 846 100.0 951 6 US-10-775-204-409
40 846 100.0 954 6 US-10-775-204-401
41 844 99.8 166 6 US-10-658-834A-959
42 844 99.8 166 6 US-10-658-834A-967
43 843 99.6 166 6 US-10-658-834A-952
44 843 99.6 166 6 US-10-658-834A-955
45 843 99.6 166 6 US-10-658-834A-958

Query Match 100.0%; Score 846; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 9.1e-82;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 APPRLICDSRVLYRLLLEAKEAENITTCAGHCSLNENITVPDTKNFYAKRMEVGQQA 60
Db 1 APPRLICDSRVLYRLLLEAKEAENITTCAGHCSLNENITVPDTKNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKKEAIS 120
QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGD 165
Db 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGD 165

RESULT 2
US-10-634-477-1
; Sequence 1, Application US/10634477
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Paul
; APPLICANT: Roediger, Ralf
; APPLICANT: Walter-Matsui, Ruth
; TITLE OF INVENTION: TREATMENT OF DISTURBANCES OF IRON DISTRIBUTION
; FILE REFERENCE: 21368
; CURRENT APPLICATION NUMBER: US/10/634,477
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: 02019100.3
; PRIOR FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-634-477-1

Query Match 100.0%; Score 846; DB 6; Length 165;
Best Local Similarity 100.0%; Pred. No. 9,1e-82;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCAGHCSLNENITVPDTKNFYAKRMEVGQQA 60
Db 1 APPRLICDSRVLYRLLLEAKEAENITTCAGHCSLNENITVPDTKNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKKEAIS 120
QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGD 165
Db 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGD 165

RESULT 3
US-10-780-297-1
; Sequence 1, Application US/10780297
; GENERAL INFORMATION:
; APPLICANT: Papadimitriou, Apollon
; TITLE OF INVENTION: Erythropoietin Composition
; FILE REFERENCE: 20619 US
; CURRENT APPLICATION NUMBER: US/10/780,297
; CURRENT FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US/09/853,731
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP/00110355.5
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-780-297-1

Query Match 100.0%; Score 846; DB 6; Length 165;
Best Local Similarity 100.0%; Pred. No. 9,1e-82;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCAGHCSLNENITVPDTKNFYAKRMEVGQQA 60
Db 1 APPRLICDSRVLYRLLLEAKEAENITTCAGHCSLNENITVPDTKNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKKEAIS 120
QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGD 165
Db 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGD 165

RESULT 4
US-10-780-297-2
; Sequence 1, Application US/10780297
; GENERAL INFORMATION:
; APPLICANT: Papadimitriou, Apollon
; TITLE OF INVENTION: Erythropoietin Composition
; FILE REFERENCE: 20619 US
; CURRENT APPLICATION NUMBER: US/10/780,297
; CURRENT FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US/09/853,731
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP/00110355.5
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-780-297-2

Query Match 100.0%; Score 846; DB 6; Length 166;
Best Local Similarity 100.0%; Pred. No. 9,1e-82;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCAGHCSLNENITVPDTKNFYAKRMEVGQQA 60
Db 1 APPRLICDSRVLYRLLLEAKEAENITTCAGHCSLNENITVPDTKNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKKEAIS 120
QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGD 165
Db 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGD 165

RESULT 5
US-10-658-834A-201
; Sequence 201, Application US/10658834A
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Dittanci, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; TITLE OF INVENTION: Acid
; TITLE OF INVENTION: Molecules and Related Applications
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
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Best Local Similarity 100.0%; Pred. No. 9,1e-82;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 APPRLICDSRVLYRLLLEAKEAENITTCAGHCSLNENITVPDTKNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKKEAIS 120
QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGD 165
Db 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGD 165

RESULT 4
US-10-780-297-2
; Sequence 1, Application US/10780297
; GENERAL INFORMATION:
; APPLICANT: Papadimitriou, Apollon
; TITLE OF INVENTION: Erythropoietin Composition
; FILE REFERENCE: 20619 US
; CURRENT APPLICATION NUMBER: US/10/780,297
; CURRENT FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US/09/853,731
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP/00110355.5
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-780-297-2

Query Match 100.0%; Score 846; DB 6; Length 166;
Best Local Similarity 100.0%; Pred. No. 9,1e-82;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCAGHCSLNENITVPDTKNFYAKRMEVGQQA 60
Db 1 APPRLICDSRVLYRLLLEAKEAENITTCAGHCSLNENITVPDTKNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKKEAIS 120
QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGD 165
Db 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGEACRTGD 165

RESULT 5
US-10-658-834A-201
; Sequence 201, Application US/10658834A
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Dittanci, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; TITLE OF INVENTION: Acid
; TITLE OF INVENTION: Molecules and Related Applications
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
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SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 201
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank AA52400
DATABASE ENTRY DATE: 1994-11-08
S-10-658-834A-201

Query Match 100.0%; Score 846; DB 6; Length 166;
Best Local Similarity 100.0%; Pred. No. 9.1e-82;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 APPRLCDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 60
b 1 APPRLCDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 60
Y 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHVDAVSGLSRLTLLRALGAQKEAIS 120
b 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHVDAVSGLSRLTLLRALGAQKEAIS 120
Y 121 PPDAASAAPLRTITADTFRKLFYVSNFRLGKLYTGACRTGD 165
b 121 PPDAASAAPLRTITADTFRKLFYVSNFRLGKLYTGACRTGD 165

RESULT 6

US-10-773-939-2
Sequence 2, Application US/10773939
GENERAL INFORMATION:
APPLICANT: Cox III, George N
APPLICANT: Bolder Biotechnology, Inc.
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REFERENCE: 4152-1-PUS
CURRENT APPLICATION NUMBER: US/10773,939
CURRENT FILING DATE: 2004-02-05
PRIOR FILING DATE: US/10/400,377
PRIOR FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/052,516
PRIOR FILING DATE: 1997-07-14
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
US-10-773-939-2

Query Match 100.0%; Score 846; DB 6; Length 166;
Best Local Similarity 100.0%; Pred. No. 9.1e-82;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 APPRLCDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 60
b 1 APPRLCDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 60
Y 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHVDAVSGLSRLTLLRALGAQKEAIS 120
b 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHVDAVSGLSRLTLLRALGAQKEAIS 120
Y 121 PPDAASAAPLRTITADTFRKLFYVSNFRLGKLYTGACRTGD 165
b 121 PPDAASAAPLRTITADTFRKLFYVSNFRLGKLYTGACRTGD 165

RESULT 7

US-10-774-149-2
Sequence 2, Application US/10774149
GENERAL INFORMATION:
APPLICANT: Cox III, George N

APPLICANT: Bolder Biotechnology, Inc.
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REFERENCE: 4152-1-PUS
CURRENT APPLICATION NUMBER: US/10/774,149
CURRENT FILING DATE: 2004-02-05
PRIOR FILING DATE: US/10/400,377
PRIOR FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/052,516
PRIOR FILING DATE: 1997-07-14
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
US-10-774-149-2

Query Match 100.0%; Score 846; DB 6; Length 166;
Best Local Similarity 100.0%; Pred. No. 9.1e-82;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 APPRLCDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 60
b 1 APPRLCDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 60
Y 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHVDAVSGLSRLTLLRALGAQKEAIS 120
b 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHVDAVSGLSRLTLLRALGAQKEAIS 120
Y 121 PPDAASAAPLRTITADTFRKLFYVSNFRLGKLYTGACRTGD 165
b 121 PPDAASAAPLRTITADTFRKLFYVSNFRLGKLYTGACRTGD 165

RESULT 8

US-10-775-204-593
Sequence 593, Application US/10775204
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Haseltine, William A.
APPLICANT: Balance, David J.
APPLICANT: Turner, Andrew J.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF564
CURRENT APPLICATION NUMBER: US/10/775,204
CURRENT FILING DATE: 2004-02-11
PRIOR FILING DATE: 60/341,811
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/360,000
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/378,950
PRIOR FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: 60/398,008
PRIOR FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: 60/411,355
PRIOR FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: 60/414,984
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: 60/417,611
PRIOR FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 60/420,246
PRIOR FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: 60/423,623
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/351,360
PRIOR FILING DATE: 2002-01-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2222
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 593
LENGTH: 192

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/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-775-204-593

Query Match      100.0%; Score 846; DB 6; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.1e-81;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKAEENITTCABHCSLNENITVPDTKKNFYAKRMEVGQQA 60
DB 28 APPRLICDSRVLYRLLLEAKAEENITTCABHCSLNENITVPDTKKNFYAKRMEVGQQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKQEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKQEAIS 147

QY 121 PPDAASAAPLRTITADTRFKLFRVYSNFRGKGLKLYTGEACRTGD 165
DB 148 PPDAASAAPLRTITADTRFKLFRVYSNFRGKGLKLYTGEACRTGD 192

RESULT 9
US-10-775-204-594
/ Sequence 594, Application US/10775204
/ GENERAL INFORMATION:
/ APPLICANT: Rosen, Craig A.
/ APPLICANT: Haseltine, William A.
/ APPLICANT: Balance, David J.
/ APPLICANT: Turner, Andrew J.
/ TITLE OF INVENTION: Albumin Fusion Proteins
/ FILE REFERENCE: PFS64
/ CURRENT APPLICATION NUMBER: US/10/775,204
/ CURRENT FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/341,811
/ PRIOR FILING DATE: 2001-12-21
/ PRIOR APPLICATION NUMBER: 60/360,000
/ PRIOR FILING DATE: 2002-02-28
/ PRIOR APPLICATION NUMBER: 60/378,950
/ PRIOR FILING DATE: 2002-05-10
/ PRIOR APPLICATION NUMBER: 60/398,008
/ PRIOR FILING DATE: 2002-07-24
/ PRIOR APPLICATION NUMBER: 60/411,355
/ PRIOR FILING DATE: 2002-09-18
/ PRIOR APPLICATION NUMBER: 60/414,984
/ PRIOR FILING DATE: 2002-10-02
/ PRIOR APPLICATION NUMBER: 60/417,611
/ PRIOR FILING DATE: 2002-10-11
/ PRIOR APPLICATION NUMBER: 60/420,246
/ PRIOR FILING DATE: 2002-10-23
/ PRIOR APPLICATION NUMBER: 60/423,623
/ PRIOR FILING DATE: 2002-11-05
/ PRIOR APPLICATION NUMBER: 60/351,360
/ PRIOR FILING DATE: 2002-01-28
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 2222
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 594
/ LENGTH: 192
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-775-204-594

Query Match      100.0%; Score 846; DB 6; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.1e-81;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKAEENITTCABHCSLNENITVPDTKKNFYAKRMEVGQQA 60
DB 28 APPRLICDSRVLYRLLLEAKAEENITTCABHCSLNENITVPDTKKNFYAKRMEVGQQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKQEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKQEAIS 147

QY 121 PPDAASAAPLRTITADTRFKLFRVYSNFRGKGLKLYTGEACRTGD 165
DB 148 PPDAASAAPLRTITADTRFKLFRVYSNFRGKGLKLYTGEACRTGD 192

RESULT 11
US-10-775-204-1689
/ Sequence 1689, Application US/10775204
/ GENERAL INFORMATION:
/ APPLICANT: Rosen, Craig A.
/ APPLICANT: Haseltine, William A.
/ APPLICANT: Balance, David J.
/ APPLICANT: Turner, Andrew J.
/ TITLE OF INVENTION: Albumin Fusion Proteins
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FILE REFERENCE: PF564
CURRENT APPLICATION NUMBER: US/10/775,204
CURRENT FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/341,811
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/360,000
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/378,950
PRIOR FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: 60/398,008
PRIOR FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: 60/411,355
PRIOR FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: 60/414,984
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: 60/417,611
PRIOR FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 60/420,246
PRIOR FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: 60/423,623
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/351,360
PRIOR FILING DATE: 2002-01-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2222
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1689
LENGTH: 192
TYPE: PRT
ORGANISM: Homo sapiens
US-10-775-204-1689

Query Match 100.0%; Score 846; DB 6; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.1e-81;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 1 APPLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPTKVNFWAKRMEVGGQA 60
2b 28 APPLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPTKVNFWAKRMEVGGQA 87
2Y 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHLVDKAVSGLSRLTLLRALGAQKEAIS 120
2b 88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHLVDKAVSGLSRLTLLRALGAQKEAIS 147
2Y 121 PPDAASAAPLRTITADTFKLFVYSNFRGLKLYTGEACRTGD 165
2b 148 PPDAASAAPLRTITADTFKLFVYSNFRGLKLYTGEACRTGD 192

RESULT 12
US-10-775-204-1690
Sequence 1690, Application US/10775204
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Haseltine, William A.
APPLICANT: Balance, David J.
APPLICANT: Turner, Andrew J.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF564
CURRENT APPLICATION NUMBER: US/10/775,204
CURRENT FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/341,811
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/360,000
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/378,950
PRIOR FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: 60/398,008
PRIOR FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: 60/411,355
PRIOR FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: 60/414,984
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: 60/417,611
PRIOR FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 60/420,246
PRIOR FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: 60/423,623
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/351,360
PRIOR FILING DATE: 2002-01-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2222
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1691
LENGTH: 192
TYPE: PRT
ORGANISM: Homo sapiens
US-10-775-204-1691

PRIOR APPLICATION NUMBER: 60/417,611
PRIOR FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 60/420,246
PRIOR FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: 60/423,623
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/351,360
PRIOR FILING DATE: 2002-01-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2222
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1690
LENGTH: 192
TYPE: PRT
ORGANISM: Homo sapiens
US-10-775-204-1690

Query Match 100.0%; Score 846; DB 6; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.1e-81;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPTKVNFWAKRMEVGGQA 60
Db 28 APPLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPTKVNFWAKRMEVGGQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHLVDKAVSGLSRLTLLRALGAQKEAIS 120
Db 88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHLVDKAVSGLSRLTLLRALGAQKEAIS 147
QY 121 PPDAASAAPLRTITADTFKLFVYSNFRGLKLYTGEACRTGD 165
Db 148 PPDAASAAPLRTITADTFKLFVYSNFRGLKLYTGEACRTGD 192

RESULT 13
US-10-775-204-1691
Sequence 1691, Application US/10775204
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Haseltine, William A.
APPLICANT: Balance, David J.
APPLICANT: Turner, Andrew J.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF564
CURRENT APPLICATION NUMBER: US/10/775,204
CURRENT FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/341,811
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/360,000
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/378,950
PRIOR FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: 60/398,008
PRIOR FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: 60/411,355
PRIOR FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: 60/414,984
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: 60/417,611
PRIOR FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 60/420,246
PRIOR FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: 60/423,623
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/351,360
PRIOR FILING DATE: 2002-01-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2222
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1691
LENGTH: 192
TYPE: PRT
ORGANISM: Homo sapiens
US-10-775-204-1691

US-10-775-204-1691

Query Match 100.0%; Score 846; DB 6; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.1e-81;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLELYLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
Db 28 APPRLICDSRVLELYLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHVDAKAVSGLSLTLRLALGAQKEAIS 120
Db 88 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHVDAKAVSGLSLTLRLALGAQKEAIS 147
QY 121 PPDAASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGD 165
Db 148 PPDAASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGD 192

RESULT 14

US-10-775-204-1828
; Sequence 1828, Application US/10775204
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Haseltine, David J.
; APPLICANT: Turner, Andrew J.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/10/775,204
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 60/423,623
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/351,360
; PRIOR FILING DATE: 2002-01-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1828
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-775-204-1828

Query Match 100.0%; Score 846; DB 6; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.1e-81;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLELYLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
Db 28 APPRLICDSRVLELYLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHVDAKAVSGLSLTLRLALGAQKEAIS 120
Db 88 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHVDAKAVSGLSLTLRLALGAQKEAIS 147
QY 121 PPDAASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGD 165

Db 148 PPDAASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGD 192

RESULT 15

US-10-775-204-1829
; Sequence 1829, Application US/10775204
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Haseltine, William A.
; APPLICANT: Balance, David J.
; APPLICANT: Turner, Andrew J.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/10/775,204
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 60/423,623
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/351,360
; PRIOR FILING DATE: 2002-01-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1829
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-775-204-1829

Query Match 100.0%; Score 846; DB 6; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.1e-81;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLELYLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
Db 28 APPRLICDSRVLELYLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHVDAKAVSGLSLTLRLALGAQKEAIS 120
Db 88 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHVDAKAVSGLSLTLRLALGAQKEAIS 147
QY 121 PPDAASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGD 165
Db 148 PPDAASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGD 192

Search completed: May 25, 2004, 11:27:56
Job time : 21 secs

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JM protein - protein search, using sw model

run on: May 25, 2004, 11:15:48 ; Search time 18 seconds

(without alignments)
477,310 Million cell updates/sec

title: US-09-830-964-1

perfect score: 846

sequence: 1 APRRLICDSRVLYLEAK.....SNFLRGKLYTGEARTCD 165

scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	759.5	89.8	192	1	P07865 macaca fasc
4	706	83.5	192	1	Q28513 macaca mula
5	701	82.9	192	1	P33708 felis silve
6	692.5	81.9	192	1	P29676 rattus norv
7	689	81.4	192	1	P48617 bos taurus
8	685.5	80.1	194	1	P07321 mus muscullu
9	678	80.1	190	1	P33709 ovis aries
10	638	75.4	175	1	P49157 sus scrofa
11	109	12.9	352	1	P33707 canis famil
12	89	10.5	353	1	P42705 canis famil
13	83	9.8	339	1	P40245 homo sapien
14	82	9.7	548	1	Q9hzm7 pseudomonas
15	80.5	9.5	3033	1	Q8kix4 buchnera ap
16	78.5	9.3	897	1	P26661 h genome po
17	78	9.2	548	1	P42567 mus muscullu
18	78	9.2	548	1	Q59177 buchnera ap
19	78	9.2	747	1	Q32n35 buchnera ap
20	77	9.1	548	1	P37279 synechococc
21	76.5	9.0	386	1	O51832 buchnera ap
22	76.5	9.0	545	1	O46036 drosophila
23	75	8.9	545	1	Q88n55 pseudomonas
24	75	8.9	548	1	O8cx48 shewanella
25	74.5	8.8	552	1	Q3n334 buchnera ap
26	74.5	8.8	809	1	Q33500 pseudomonas
27	74	8.7	326	1	P37024 escherichia
28	74	8.7	551	1	P49745 rattus norv
29	74	8.7	1564	1	Q8kix0 buchnera ap
30	73.5	8.7	830	1	P51533 saccharomyc
31	73.5	8.7	837	1	Q9jbd2 mus muscullu
32	73	8.6	283	1	O92830 homo sapien
33	73	8.6	1089	1	O83030 deinoxocous
					P32337 saccharomyc

ALIGNMENTS

RESULT 1

EPO_HUMAN

ID EPO_HUMAN STANDARD; PRT; 193 AA.

AC P01588; Q9UDZ0; Q9UEZ5; Q9UHA0;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Erythropoietin precursor (Epoetin).

GN EPO.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=85137899; PubMed=3838366;

RA Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J.,

RA Musson A., Seehra J., Jones S.S., Hewick R., Fritsch E.F.,

RA Kawakita M., Shimizu T., Miyake T.;

RT "Isolation and characterization of genomic and cDNA clones of human

RT erythropoietin.";

RL Nature 313:806-810(1985).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=86067948; PubMed=3865178;

RA Lin F.-K., Suggs S., Lin C.-H., Browne J.K., Smalling R., Egrie J.C.,

RA Cher K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai P.-H.,

RA Goldwasser E.;

RT "Cloning and expression of the human erythropoietin gene.";

RL Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=99018118; PubMed=9799793;

RA Gloeckner G., Scherer S., Schattevoy R., Boright A.P., Weber J.,

RA Tsui L.-C., Rosenthal A.;

RT "Large-scale sequencing of two regions in human chromosome 7q22:

RT analysis of 650 kb of genomic sequence around the EPO and CUTL1 loci

RT reveals 17 genes.";

RL Genome Res. 8:1060-1073(1998).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=93384593; PubMed=8396923;

RA Funakoshi A., Muta H., Baba T., Shimizu S.;

RT "Gene expression of mutant erythropoietin in hepatocellular

RT carcinoma.";

RL Biochem. Biophys. Res. Commun. 195:717-722(1993).

RN [5]

RP SEQUENCE OF 58-193 FROM N.A., AND VARIANTS HEPATOCELLULAR CARCINOMA

RP 131-ASN-PHE-132 AND GLN-149.

RX MEDLINE=93384593; PubMed=8396923;

RA Funakoshi A., Muta H., Baba T., Shimizu S.;

RT "Gene expression of mutant erythropoietin in hepatocellular

RT carcinoma.";

RL Biochem. Biophys. Res. Commun. 195:717-722(1993).

RN [6]

RP SEQUENCE OF 28-193, AND DISULFIDE BONDS.

RP TISSUE=Urine;

RC

RX MEDLINE=86140080; PubMed=3949763;
RA Lai P.H., Everett R., Wang F.F., Arakawa T., Goldwasser E.,
RT "Structural characterization of human erythropoietin.";
RL J. Biol. Chem. 261:3116-3121(1986).
RN [7]
RP PRELIMINARY SEQUENCE OF 28-57.
RX MEDLINE=84135751; PubMed=6698989;
RA Yanggawa S., Hirade K., Omota H., Sasaki R., Chiba K., Ueda M.,
RT "Isolation of human erythropoietin with monoclonal antibodies.";
RL J. Biol. Chem. 259:2707-2710(1984).
RN [8]
RP STRUCTURE OF CARBOHYDRATES.
RX MEDLINE=88153657; PubMed=3346214;
RA Takeuchi M., Takasaki S., Miyazaki H., Kato T., Hoshi S., Kochibe N.,
RT "Comparative study of the asparagine-linked sugar chains of human
erythropoietins purified from urine and the culture medium of
recombinant Chinese hamster ovary cells.";
RL J. Biol. Chem. 263:3657-3663(1988).
RN [9]
RP STRUCTURE OF CARBOHYDRATES.
RX MEDLINE=89118279; PubMed=3219367;
RA Sasaki H., Ochi N., Dell A., Fukuda M.;
RT "Site-specific glycosylation of human recombinant erythropoietin:
analysis of glycopeptides or peptides at each glycosylation site by
fast atom bombardment mass spectrometry.";
RL Biochem.stry 27:8618-8626(1988).
RN [10]
RP STRUCTURE OF CARBOHYDRATES.
RX MEDLINE=92314463; PubMed=1820196;
RA Takeuchi M., Kobata A.;
RT "Structures and functional roles of the sugar chains of human
erythropoietins.";
RL Glycobiology 1:337-346(1991).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=98445092; PubMed=9774108;
RA Syed R.S., Reid S.W., Li C., Cheestam J.C., Aoki K.H., Liu B.,
RT "Structure of human erythropoietin at 1.9 Å resolution: implications
for receptor orientation.";
RL Nature 395:511-516(1998).
RN [12]
RP FUNCTION: Erythropoietin is the principal hormone involved in the
regulation of erythrocyte differentiation and the maintenance of a
physiological level of circulating erythrocyte mass.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
and by liver of fetal or neonatal mammals.
CC -1- PHARMACEUTICAL: Used for the treatment of anemia. Available under
the names Epogen (Amgen), Epogin (Chugai), Epomax (Eli Lilly), Eprex
(Janssen-Cilag), Neorecormon or Recormon (Roche), and Procrit
(Ortho Biotech). Variations in the glycosylation pattern of EPO
distinguish these products. Epogen, Epogin, Eprex and Procrit
are generically known as epoetin alfa, Neorecormon and Recormon as
epoetin beta and Epomax as epoetin omega.
CC -1- SIMILARITY: Belongs to the EPO / TPO family.
CC -1- DATABASE: NAME=RED Systems, cytokine source book: EPO;
WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=197".
CC -----
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CC -----
DR EMBL; X02158; CAA26095.1; --
DR EMBL; X02157; CAA26094.1; --
DR EMBL; M11319; AAA52400.1; --

DR EMBL; AF053356; AAC78791.1; --
DR EMBL; AF202308; AAF23132.1; --
DR EMBL; AF202306; AAF23132.1; JOINED.
DR EMBL; AF202307; AAF23132.1; JOINED.
DR EMBL; AF202310; AAF23133.1; --
DR EMBL; AF202309; AAF23133.1; JOINED.
DR EMBL; AF202311; AAF17572.1; --
DR EMBL; AF202314; AAF23134.1; --
DR EMBL; AF202312; AAF23134.1; JOINED.
DR EMBL; AF202313; AAF23134.1; JOINED.
DR EMBL; S65458; AAD13964.1; --
DR PIR; A01855; ZUHU.
DR PDB; 1EER; 01-OCT-99.
DR PDB; 1CN4; 11-AUG-99.
DR PDB; 1BU1; 10-SEP-99.
DR GlycoSuiteDB; P01588; --
DR Genew; HGNC:3415; EPO.
DR MIM; 133170; --
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0006950; P:response to stress; TAS.
DR InterPro; IPR001323; EPO TPO.
DR InterPro; IPR003013; Erythroptn.
DR Pfam; PF00758; EPO TPO; 1
DR PRINTS; PR00272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
KW Erythrocyte maturation; Glycoprotein; Hormone; Signal; Pharmaceutical;
KW 3D-structure; Polymorphism.
FT SIGNAL 1 27
FT CHAIN 28 193 ERYTHROPOIETIN.
FT PROPEP 190 193 MAY BE REMOVED IN PROCESSED PROTEIN.
FT DISULFID 34 188
FT DISULFID 56 60
FT CARBOHYD 51 51
FT CARBOHYD 65 65
FT CARBOHYD 110 110
FT CARBOHYD 153 153
FT VARIANT 131 132
FT VARIANT 149 149
FT CONFLICT 40 40
FT CONFLICT 85 85
FT CONFLICT 140 140
FT HELIX 32 34
FT HELIX 36 52
FT HELIX 53 55
FT TURN 57 58
FT STRAND 61 68
FT STRAND 73 73
FT HELIX 75 78
FT TURN 79 80
FT HELIX 83 109
FT HELIX 118 138
FT TURN 139 140
FT HELIX 141 147
FT TURN 148 149
FT STRAND 160 164
FT HELIX 165 177
FT TURN 178 178
FT HELIX 179 188
SQ SEQUENCE 193 AA; 21306 MW; C91F0E4C26A52033 CRC64;
Query Match 100.0%; Score 846; DB 1; Length 193;
Best Local Similarity 100.0%; Pred.No. 6.5e-74;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLICDSRLVRLYLEAKAEENITTCGAHCNSLNENITVPDTKWNFYAKRWVEVGQQA 60
DB 28 APPRLICDSRLVRLYLEAKAEENITTCGAHCNSLNENITVPDTKWNFYAKRWVEVGQQA 87

61 VEVWQGLALLSEAVLRQALLVNSOPWEPLOLHVDKAVSGLRSITTLRALGAQKEAIS 120
 88 VEVWQGLALLSEAVLRQALLVNSOPWEPLOLHVDKAVSGLRSITTLRALGAQKEAIS 147
 121 PPDAASAAPLRTITADTFKRLFRVYNSFLRGKLYTGACRTGD 165
 148 PPDAASAAPLRTITADTFKRLFRVYNSFLRGKLYTGACRTGD 192

RESULT 2

ID EPO_MACFA STANDARD; PRT; 192 AA.
 AC P07865;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Erythropoietin precursor.
 GN EPO.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 NCBI_TaxID=9541;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=87055236; PubMed=2877922;
 RC Lin F.-K., Lin C.-H., Lai P.-H., Browne J.K., Egrie J.C., Smalling R.,
 RA Fox G.M., Chen K.K., Castro M., Suggs S.;
 RT "Monkey erythropoietin gene: cloning, expression and comparison with
 the human erythropoietin gene.";
 RL Gene 44:201-209(1986).
 CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
 regulation of erythrocyte differentiation and the maintenance of a
 physiological level of circulating erythrocyte mass.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 and by liver of fetal or neonatal mammals.
 CC -!- SIMILARITY: Belongs to the EPO / TPO family.
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EMBL; M18189; AAA36841.1; -.
 PIR; JQ0173; JQ0173.
 DR HSSP; P01588; 1CN4.
 DR InterPro; IPR001323; EPO TPO.
 DR Pfam; PF00758; EPO TPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO TPO; 1.
 KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 192
 FT DISULFID 34 187
 FT CARBOHYD 56 60
 FT CARBOHYD 51 51
 FT CARBOHYD 65 65
 FT CARBOHYD 110 110
 FT CARBOHYD 152 152
 FT CARBOHYD 152 152
 SEQUENCE 192 AA; 21113 MW; EBA900F442AD4522 CRC64;
 Query Match 90.4%; Score 764.5; DB 1; Length 192;
 Best Local Similarity 91.5%; Pred. No. 4.4e-66;
 Matches 151; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

1 APPRLICDSRVLYRLLLEAKEAENITVTGCAHCSLNENITVPTKYNFYAWKRMVGGQA 60
 120 147

Db 28 APPRLICDSRVLYRLLLEAKEAENITVTGCAHCSLNENITVPTKYNFYAWKRMVGGQA 87
 Qy 61 VEVWQGLALLSEAVLRQALLVNSOPWEPLOLHVDKAVSGLRSITTLRALGAQKEAIS 120
 Db 88 VEVWQGLALLSEAVLRQALLVNSOPWEPLOLHVDKAVSGLRSITTLRALGAQKEAIS 146
 Qy 121 PPDAASAAPLRTITADTFKRLFRVYNSFLRGKLYTGACRTGD 165
 Db 147 PPDAASAAPLRTITADTFKRLFRVYNSFLRGKLYTGACRTGD 191

RESULT 3

ID EPO_MACMU STANDARD; PRT; 192 AA.
 AC Q28513;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Erythropoietin precursor.
 GN EPO.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 NCBI_TaxID=9544;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=93372347; PubMed=8364201;
 RC Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
 RA Czelusniak J., Goodman M., Bunn H.F.;
 RT "Erythropoietin structure-function relationships: high degree of
 sequence homology among mammals.";
 RL Blood 82:1507-1516(1993).
 CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
 regulation of erythrocyte differentiation and the maintenance of a
 physiological level of circulating erythrocyte mass.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 and by liver of fetal or neonatal mammals.
 CC -!- SIMILARITY: Belongs to the EPO / TPO family.
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EMBL; L10609; AAA36842.1; -.
 PIR; I84613; I84613.
 DR HSSP; P01588; 1CN4.
 DR InterPro; IPR001323; EPO TPO.
 DR Pfam; PF00758; EPO TPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO TPO; 1.
 KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 192
 FT DISULFID 34 187
 FT CARBOHYD 56 60
 FT CARBOHYD 51 51
 FT CARBOHYD 65 65
 FT CARBOHYD 110 110
 FT CARBOHYD 152 152
 SEQUENCE 192 AA; 21081 MW; 275560A264628CD1 CRC64;
 Query Match 89.8%; Score 759.5; DB 1; Length 192;
 Best Local Similarity 90.3%; Pred. No. 1.2e-65;
 Matches 149; Conservative 9; Mismatches 6; Indels 1; Gaps 1;

QY 1 APPRLICDSRVLYRLLLEAKAEANITGCAEHCSLNENITVPTDKVNFYAKMEVGGQA 60
DB 28 APPRLVCDSDRVLYRLLLEAKAEANITVPTDKVNFYAKMEVGGQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVDAKAVSLRSLTLLRACGAQKEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVDAKAVSLRSLTLLRACGAQKEAIS 146
QY 121 PPDAAASAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGD 165
DB 147 LPDAAASAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGD 191

RESULT 4
EPO_FELCA
ID EPO_FELCA STANDARD; PRT; 192 AA.
AC P33708;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Erythropoietin precursor.
GN EPO.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Goodman R.E., Bell R.G.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE OF 5-192 FROM N.A.
RX MEDLINE=93372347; PubMed=8364201;
RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
RA Czelusniak J., Goodman M., Bunn H.F.;
RT "Erythropoietin structure-function relationships: high degree of
RT sequence homology among mammals.";
RL Blood 82:1507-1516(1993).
CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
CC regulation of erythrocyte differentiation and the maintenance of a
CC physiological level of circulating erythrocyte mass.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC and by liver of fetal or neonatal mammals.
CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
CC and by liver of fetal or neonatal mammals.
CC -!- SIMILARITY: Belongs to the EPO / TPO family.
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CC
CC ENBL; U00685; AAA18282.1; -;
CC ENBL; L10606; AAA30807.1; -;
CC PIR; I46083; I46083.
CC HSP; P01588; 1CN4.
CC InterPro: IPR001323; EPO TPO.
CC Pfam: PF00758; EPO TPO; 1.
CC PRINTS; PR00272; ERYTHROPTN.
CC PROSITE; PS00817; EPO_TPO; 1.
KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
FT SIGNAL 1 26
FT CHAIN 27 192
FT DISULFID 33 187
FT DISULFID 55 59
FT CARBOHYD 50 50
FT CARBOHYD 64 64
FT CARBOHYD 109 109
FT CONFLICT 44 44
FT G -> E (IN REF. 2).

QY 1 APPRLICDSRVLYRLLLEAKAEANITGCAEHCSLNENITVPTDKVNFYAKMEVGGQA 60
DB 27 APPRLICDSRVLYRLLLEAKAEANITVPTDKVNFYAKMEVGGQA 86
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVDAKAVSLRSLTLLRACGAQKEAIS 120
DB 87 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVDAKAVSLRSLTLLRACGAQKEAIS 146
QY 121 PPDAAASAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGD 165
DB 147 LPEATSAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGD 191

RESULT 5
EPO_RAT
ID EPO_RAT STANDARD; PRT; 192 AA.
AC P29576; P70504;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Erythropoietin precursor.
GN EPO.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Kidney;
RX MEDLINE=93042015; PubMed=1420369;
RA Nagao M., Suga H., Okano M., Masuda S., Narita H., Ikura K.,
RA Sasaki R.;
RT "Nucleotide sequence of rat erythropoietin.";
RL Biochim. Biophys. Acta 1171:99-102(1992).
RN [2]
RP SEQUENCE OF 4-192 FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
RX MEDLINE=93372347; PubMed=8364201;
RA Wen D., Boissel J.P.R., Tracy T.E., Mulcahy L.S., Czelusniak J.,
RA Goodman M., Bunn H.F.;
RT "Erythropoietin structure-function relationships: high degree of
RT sequence homology among mammals.";
RL Blood 82:1507-1516(1993).
CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
CC regulation of erythrocyte differentiation and the maintenance of a
CC physiological level of circulating erythrocyte mass.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
CC and by liver of fetal or neonatal mammals.
CC -!- SIMILARITY: Belongs to the EPO / TPO family.
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CC
CC ENBL; D10763; BAA01593.1; -;
CC ENBL; L10608; AAA41126.1; -;
CC PIR; S28148; S28148.
CC HSP; P01588; 1CN4.
CC InterPro: IPR001323; EPO TPO.
CC InterPro: IPR003013; Erythroptn.
CC Pfam: PF00758; EPO_TPO; 1.
CC PRINTS; PR00272; ERYTHROPTN.
CC

RT G- protein beta2 subunit gene and the Epo gene.;"

RL Oncogene 15:1995-1999(1997);

CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the

CC regulation of erythrocyte differentiation and the maintenance of a

CC physiological level of circulating erythrocyte mass.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals

CC and by liver of fetal or neonatal mammals.

CC -!- SIMILARITY: Belongs to the EPO / TPO family.

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CC

DR EMBL; M12482; AAA37568.1; -

DR EMBL; M12930; AAA37570.1; -

DR EMBL; AF312033; AAK28825.1; -

DR EMBL; Y11971; CAA72707.1; -

DR PIR; A24902; A24902.

DR HSSP; P01588; 1CM4.

DR MGD; MGI:95407; Epo.

DR InterPro; IPR001323; EPO TPO.

DR InterPro; IPR003013; Erythroptn.

DR Pfam; PF00758; EPO TPO; 1.

DR PRINTS; PR00272; ERYTHROPTN.

DR PROSITE; PS00817; EPO TPO; 1.

KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.

FT SIGNAL 1 26

FT CHAIN 27 192

FT DISULFID 33 187

FT CARBOHYD 50 50 N-LINKED (GLCNAC. .) (BY SIMILARITY).

FT CARBOHYD 64 64 N-LINKED (GLCNAC. .) (BY SIMILARITY).

FT CARBOHYD 109 109 N-LINKED (GLCNAC. .) (BY SIMILARITY).

SQ SEQUENCE 192 AA; 21365 MW; 65F943214E0DF2E CRC64;

Query Match 81.4%; Score 689; DB 1; Length 192;

Best Local Similarity 80.0%; Pred. No. 7.1e-59;

Matches 132; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLELYLEAKAEENITTCGAHCNSLNENITVPDTKNFYAKRMEVQQA 60

Db 27 APPRLICDSRVLELYLEAKAEENITTCGAHCNSLNENITVPDTKNFYAKRMEVEEQA 86

QY 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSRLTTLRLALGAKQKAIS 120

Db 87 IEVWQGLALLSEAILQALLANSOPPBTLLQHLIDKAIKSLRLSLTLRLVLGAKELMS 146

QY 121 PPDAAAPLRTITADTFKLFVYNSFLRGKLYTGEACRTGD 165

Db 147 PPDTPPAPLRTITADTFKLFVYNSFLRGKLYTGEVCRGD 191

RESULT 8

EPO_SHEEP STANDARD; PRT; 194 AA.

Id -EPO_SHEEP

AC P33709; Q28572;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

GN Erythropoietin precursor.

DE EPO.

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Caprinae; Ovis.

OX NCBI_TaxID=9940;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Kidney;

RX MEDLINE=93351736; PubMed=8349021;

RA Fu P., Evans B., Lim G.B., Moritz K., Wintour M.E.;

RT "The sheep erythropoietin gene: molecular cloning and effect of

RT hemorrhage on plasma erythropoietin and renal/liver messenger RNA in

RT adult sheep.;"

RL Mol. Cell. Endocrinol. 93:107-116(1993).

RN [2]

RP SEQUENCE OF 4-194 FROM N.A.

RC TISSUE-Kidney;

RX MEDLINE=93372347; PubMed=8364201;

RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,

RA Czelusniak J., Goodman M., Bunn H.F.;

RT "Erythropoietin structure-function relationships: high degree of

RT sequence homology among mammals.;"

RL Blood 82:1507-1516(1993).

CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the

CC regulation of erythrocyte differentiation and the maintenance of a

CC physiological level of circulating erythrocyte mass.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals

CC and by liver of fetal or neonatal mammals.

CC -!- SIMILARITY: Belongs to the EPO / TPO family.

CC

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CC

DR EMBL; Z24681; CRA80848.1; -

DR EMBL; L10610; AAA31518.1; -

DR PIR; I46401; I46401.

DR HSSP; P01588; 1CM4.

DR InterPro; IPR001323; EPO TPO.

DR InterPro; IPR003013; Erythroptn.

DR Pfam; PF00758; EPO TPO; 1.

DR PRINTS; PR00272; ERYTHROPTN.

DR PROSITE; PS00817; EPO TPO; 1.

KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.

FT SIGNAL 1 27

FT CHAIN 28 194

FT DISULFID 34 189

FT DISULFID 56 60 BY SIMILARITY.

FT CARBOHYD 51 51 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 65 65 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 110 110 F -> L (IN REF. 2).

FT CONFLICT 16 16 L -> P (IN REF. 2).

FT CONFLICT 108 108

SQ SEQUENCE 194 AA; 21335 MW; C025AAB0528131A9 CRC64;

Query Match 81.0%; Score 685.5; DB 1; Length 194;

Best Local Similarity 81.9%; Pred. No. 1.6e-58;

Matches 136; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 1 APPRLICDSRVLELYLEAKAEENITTCGAHCNSLNENITVPDTKNFYAKRMEVQQA 60

Db 28 APPRLICDSRVLELYLEAKAEENITTCGAHCNSLNENITVPDTKNFYAKRMEVQQA 87

QY 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSRLTTLRLALGAKQKAIS 120

Db 88 LEVWQGLALLSEAFRQALLANSQPCEALRLHVDKAVSGLSRLTTLRLALGAKQKAIP 147

QY 121 PPDAA- SAAPLRTITADTFKLFVYNSFLRGKLYTGEACRTGD 165

Db 148 LPDATSAAPLRTITADTFKLFVYNSFLRGKLYTGEACRTGD 193

RESULT 9

EPO_PIG STANDARD; PRT; 190 AA.

Id -EPO_PIG

AC P49157;

01-FEB-1996 (Rel. 33, Created)
 01-FEB-1996 (Rel. 33, Last sequence update)
 16-OCT-2001 (Rel. 40, Last annotation update)
 Erythropoietin precursor (Fragment).
 EPO.
 Sus scrofa (Pig).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxID=9823;
 [1]
 P SEQUENCE FROM N.A.
 C TISSUE=Kidney;
 X MEDLINE=93372347; PubMed=8364201;
 A Wen D., Boiesel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
 C Celueniak J., Goodman M., Bunn H.F.;
 T "Erythropoietin structure-function relationships: high degree of
 T sequence homology among mammals.";
 L Blood 82:1507-1516(1993)
 X -!- FUNCTION: Erythropoietin is the principal hormone involved in the
 X regulation of erythrocyte differentiation and the maintenance of a
 X physiological level of circulating erythrocyte mass.
 X -!- SUBCELLULAR LOCATION: Secreted.
 X -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 X and by liver of fetal or neonatal mammals.
 X -!- SIMILARITY: Belongs to the EPO / TPO family.
 X
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 X or send an email to license@isb-sib.ch).
 X
 X EMBL; L10607; AAA31029.1; -;
 X PIR; I46578; I46578.
 X HSSP; P01588; 1CN4.
 X InterPro; IPR001323; EPO.TPO.
 X InterPro; IPR003013; Erythroptn.
 X Pfam; PF00758; EPO.TPO; 1.
 X PRINTS; PR00272; ERYTHROPTN.
 X PROSITE; PS00817; EPO.TPO; 1.
 X Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 X
 X FT NON TER 1 22 POTENTIAL.
 X FT SIGNAL <1 22 ERYTHROPOIETIN.
 X FT CHAIN 23 190 BY SIMILARITY.
 X FT DISULFID 29 185 BY SIMILARITY.
 X FT DISULFID 51 55 BY SIMILARITY.
 X FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 X FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
 X FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
 X FT CARBOHYD 168 168 N-LINKED (GLCNAC. . .) (POTENTIAL).
 X SEQUENCE 190 AA; 20888 MW; A75BD6CCE5077E2A CRC64;
 X
 X Query Match 80.1%; Score 678; DB 1; Length 190;
 X Best Local Similarity 82.0%; Pred. No. 7.9e-58;
 X Matches 137; Conservative 7; Mismatches 21; Indels 2; Gaps 1;
 X
 X 1 APPRLICDSRVLERYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVQQA 60
 X 23 APPRLICDSRVLERYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVQQA 82
 X
 X 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
 X 83 MEVWQGLALLSEALIQGALLANSQSPSEALQLHVDKAVSGLSRLTLLRALGAQKEAIP 142
 X
 X 121 PDA--ASAAPLRTITADTFKLFVYNSFLRGKLYTGACHTGD 165
 X 143 LPDASPSATPRTFAVDTLCKLFVYNSFLRGKLYTGACRRD 189
 X
 X RESULT 10
 X EPO_CANFA

EPO_CANFA STANDARD; PRT; 175 AA.
 P33707;
 01-FEB-1994 (Rel. 28, Created)
 01-FEB-1994 (Rel. 28, Last sequence update)
 16-OCT-2001 (Rel. 40, Last annotation update)
 Erythropoietin precursor (Fragment).
 EPO.
 Canis familiaris (Dog).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 NCBI_TaxID=9615;
 [1]
 P SEQUENCE FROM N.A.
 X MEDLINE=93372347; PubMed=8364201;
 A Wen D., Boiesel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
 C Celueniak J., Goodman M., Bunn H.F.;
 T "Erythropoietin structure-function relationships: high degree of
 T sequence homology among mammals.";
 L Blood 82:1507-1516(1993)
 X -!- FUNCTION: Erythropoietin is the principal hormone involved in the
 X regulation of erythrocyte differentiation and the maintenance of a
 X physiological level of circulating erythrocyte mass.
 X -!- SUBCELLULAR LOCATION: Secreted.
 X -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 X and by liver of fetal or neonatal mammals.
 X -!- SIMILARITY: Belongs to the EPO / TPO family.
 X
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 X or send an email to license@isb-sib.ch).
 X
 X EMBL; L13027; AAA30842.1; -;
 X PIR; I46199; I46199.
 X HSSP; P01588; 1CN4.
 X InterPro; IPR001323; EPO.TPO.
 X InterPro; IPR003013; Erythroptn.
 X Pfam; PF00758; EPO.TPO; 1.
 X PRINTS; PR00272; ERYTHROPTN.
 X PROSITE; PS00817; EPO.TPO; 1.
 X Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 X
 X FT NON TER 1 1
 X FT SIGNAL <1 22 BY SIMILARITY.
 X FT CHAIN 23 >175 ERYTHROPOIETIN.
 X FT DISULFID 29 >175 BY SIMILARITY.
 X FT DISULFID 51 55 BY SIMILARITY.
 X FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 X FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
 X FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
 X FT NON TER 175 175
 X SEQUENCE 175 AA; 19193 MW; B504F8DB86676BF4 CRC64;
 X
 X Query Match 75.4%; Score 638; DB 1; Length 175;
 X Best Local Similarity 81.0%; Pred. No. 4.9e-54;
 X Matches 124; Conservative 13; Mismatches 16; Indels 0; Gaps 0;
 X
 X 1 APPRLICDSRVLERYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVQQA 60
 X 23 APPRLICDSRVLERYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVQQA 82
 X
 X 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
 X 83 MEVWQGLALLSEALIQGALLANSQSPSEALQLHVDKAVSGLSRLTLLRALGAQKEAIS 142
 X
 X 121 PDA--ASAAPLRTITADTFKLFVYNSFLRGKLYTGACHTGD 153
 X 143 LPDASPSATPRTFAVDTLCKLFVYNSFLRGKLYTGACRRD 175
 X
 X RESULT 11

TPO_CANFA STANDARD; PRT; 352 AA.
AC P42705;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Thrombopoietin precursor (Megakaryocyte colony stimulating factor)
DE (C-MPL ligand) (ML) (Megakaryocyte growth and development factor)
DE (MGDF)
GN THPO OR TPO
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-44.
RC TISSUE=Kidney.
RX MEDLINE=94291201; PubMed=8020099;
RA Bartley T.D., Bogenberger J., Hunt P., Li Y.-S., Lu H.S., Martin F.,
Chang M.-S., Samal B.B., Nichol J.L., Swift S., Johnson M.J.,
Hsu R.-Y., Parker V.P., Suggs S., Skrine J.D., Merewether L.A.,
Clogson C., Hsu E., Hokom M.M., Hornkohl A., Choi E., Pangellinan M.,
Sun Y., Mar V., McNich J., Simonet L., Jacobsen F., Xie C.,
Shuter J., Chute H., Basu R., Selander L., Trolinger D., Sieu L.,
Padilla D., Trail G., Elliott G., Izumi R., Covey T., Crouse J.,
Garcia A., Xu W., del Castillo J., Biron J., Cole S., Hu M.C.-T.,
Pacifci R., Ponting I., Saris C., Wen D., Yung Y.P., Lin H.,
Bosselman R.A.;
RT Identification and cloning of a megakaryocyte growth and development
factor that is a ligand for the cytokine receptor Mpl.";
RL Cell 77:1117-1117(1994).
CC -I- FUNCTION: Lineage-specific cytokine affecting the proliferation
and maturation of megakaryocytes from their committed progenitor
cells. It acts at a late stage of megakaryocyte development. It
may be the major physiological regulator of circulating platelets.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- DOMAIN: Two-domain structure with an erythropoietin-like N-
terminal and a Src/Pro/Thr-rich C-terminal.
CC -I- SIMILARITY: Belongs to the EPO / TPO family.
DR InterPro: IPR001323; EPO TPO.
DR Pfam: PF00758; EPO TPO; 1.
DR PRINTS: PR01485; THROMBOPTN.
DR PROSITE: PS00817; EPO TPO; 1.
KW Cytokine; Glycoprotein; Hormone; Signal.
FT SIGNAL 1 23
FT CHAIN 24 352 THROMBOPOIETIN.
FT DISULFID 28 172 POTENTIAL.
FT DISULFID 50 106 POTENTIAL.
FT CARBOHYD 185 185 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 206 206 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 255 255 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 347 347 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 352 AA; 37641 MW; 024F3B41B061FBD8 CRC64;

Query Match 12.9%; Score 109; DB 1; Length 352;
Best Local Similarity 24.0%; Pred. No. 0.0054;
Matches 40; Conservative 23; Mismatches 62; Indels 42; Gaps 5;
QY 1 APPRLTCDSRVLEYLEAKEAENITTCGAECSCSNENITVPDTKNFYAMKRMVGGQA 60
DB 24 APP-ACDPELLNKMRLDSHVLSRLSCPDYPLSTFTVLLPAVDLSLGKWTKEQTKA 81
QY 61 VEVWQGLALSLAVL--RQALLVNSQWPEPLQHVDKVSGRLSLTTLRALCAQKEA 118
DB 82 QDVGAVALLDGVLAARQQL-----GPSCLSSLLGQLSGQVRL 120
QY 119 I-----SPDAAASAPLRTITADTFKFLFRVYSNFLRGK 154
DB 121 LIGALQQLIGTQLPFG-----RTTHKDPNAIFLSFQQLRGKVR 161

RESULT 12
TPO_HUMAN STANDARD; PRT; 353 AA.
ID TPO_HUMAN
AC P40225; Q13020; Q15790; Q15791; Q15792;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Thrombopoietin precursor (Megakaryocyte colony stimulating factor)
DE (Myeloproliferative leukemia virus oncogene ligand) (C-mpl ligand)
DE (ML) (Megakaryocyte growth and development factor) (MGDF).
GN THPO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Fetal liver;
RX MEDLINE=94261202; PubMed=8202154;
RA de Sauvage F.J., Haas P.E., Spencer S.D., Malloy B.E., Gurney A.L.,
Spencer S.A., Darbonne W.C., Henzel W.J., Wong S.C., Kuang W.-J.,
Oles K.J., Hultgren B., Solberg L.A. Jr., Gosdel D.V., Eaton D.L.,
"Stimulation of megakaryocytopoiesis and thrombopoiesis by the c-Mpl
ligand.";
RL Nature 369:533-538(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Fetal liver;
RX MEDLINE=94291201; PubMed=8020099;
RA Bartley T.D., Bogenberger J., Hunt P., Li Y.-S., Lu H.S., Martin F.,
Chang M.-S., Samal B.B., Nichol J.L., Swift S., Johnson M.J.,
Hsu R.-Y., Parker V.P., Suggs S., Skrine J.D., Merewether L.A.,
Clogson C., Hsu E., Hokom M.M., Hornkohl A., Choi E., Pangellinan M.,
Sun Y., Mar V., McNich J., Simonet L., Jacobsen F., Xie C.,
Shuter J., Chute H., Basu R., Selander L., Trolinger D., Sieu L.,
Padilla D., Trail G., Elliott G., Izumi R., Covey T., Crouse J.,
Garcia A., Xu W., del Castillo J., Biron J., Cole S., Hu M.C.-T.,
Pacifci R., Ponting I., Saris C., Wen D., Yung Y.P., Lin H.,
Bosselman R.A.;
RT Identification and cloning of a megakaryocyte growth and development
factor that is a ligand for the cytokine receptor Mpl.";
RL Cell 77:1117-1124(1994).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95108091; PubMed=7809166;
RA Foster D.C., Spracher C.A., Grant F.J., Kramer J.M., Kuijper J.L.,
Holly R.D., Whitmore T.E., Heipel M.D., Bell L.A.N., Ching A.F.,
McGrane V., Hart C., O'Hara P.J., Lok S.,
"Human thrombopoietin: gene structure, cDNA sequence, expression, and
chromosomal localization.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:13023-13027(1994).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95010765; PubMed=7926023;
RA Sohma Y., Akahori H., Seki N., Hori T.-A., Ogami K., Kawamura K.,
Miyazaki H.;
RT "Molecular cloning and chromosomal localization of the human
thrombopoietin gene.";
RL FEBS Lett. 353:57-61(1994).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=95152076; PubMed=7849319;
RA Gurney A.L., Kuang W.-J., Xie M.-H., Malloy B.E., Eaton D.L.,
de Sauvage F.J.;
RT "Genomic structure, chromosomal localization, and conserved
alternative splice forms of thrombopoietin.";
RL Blood 85:981-988(1995).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Liver;
RX MEDLINE=96015174; PubMed=8537317;

Kato T., Ogami K., Shimada Y., Iwamatsu A., Sohma Y., Akahori H.,
 Horie K., Kokubo A., Kudo Y., Maeda E., Kobayashi K., Ohashi H.,
 Ozawa T., Inoue H., Kawamura K., Miyazaki H.,
 "Purification and characterization of thrombopoietin."
 J. Biochem. 118:223-236(1995).
 [7]
 SEQUENCE FROM N.A. (ISOFORM 1).
 TISSUE=Placenta;
 MEDLINE=9512248; PubMed=7822271;
 Chang M., McIninch J., Basu R., Shutter J., Heu R., Perkins C., Mar V.,
 Suggs S., Welcher A., Li L., Lu H., Bartley T., Hunt P., Martin F.,
 Samal B., Bogenberger J.,
 "Cloning and characterization of the human megakaryocyte growth and
 development factor (MGDF) gene."
 J. Biol. Chem. 270:511-514(1995).
 [8]
 SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
 Im S.H., Lee W.S., Chung K.H.;
 "Cloning and sequencing of human thrombopoietin."
 Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 -!- FUNCTION: Lineage-specific cytokine affecting the proliferation
 and maturation of megakaryocytes from their committed progenitor
 cells. It acts at a late stage of megakaryocyte development. It
 may be the major physiological regulator of circulating platelets.
 -!- SUBCELLULAR LOCATION: Secreted.
 -!- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=3;
 Name=1;
 IsoId=P40225-1; Sequence=displayed;
 Name=2; Synonyms=TPO-2;
 IsoId=P40225-2; Sequence=WSP_001450;
 Name=3; Synonyms=Truncated;
 IsoId=P40225-3; Sequence=WSP_001451;
 -!- DOMAIN: Two-domain structure with an erythropoietin-like N-
 terminal and a Ser/Pro-Thr-rich C-terminal.
 -!- SIMILARITY: Belongs to the EPO / TPO family.
 -!- DATABASE: NAME=R&D Systems' cytokine source book: TPO;
 WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=225".

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EMBL; L33410; AAA59857.1; -
 EMBL; U11025; AAA50553.1; -
 EMBL; L36051; AAC37568.1; -
 EMBL; L36052; AAC37566.1; -
 EMBL; D32046; BAA06807.1; -
 EMBL; S76771; AAB33390.1; -
 EMBL; D32047; BAA21930.1; -
 EMBL; U59493; AAB03392.1; -
 EMBL; U59494; AAB03393.1; -
 EMBL; U59495; AAB03394.1; -
 EMBL; U17071; AAX74083.1; -
 F1R; I59281; I80105.
 Genew; HGNC:11795; THPO.

MIM; 600044; -
 GO; GO:0008083; P:growth factor activity; TAS.
 GO; GO:0008283; P:cell proliferation; TAS.
 GO; GO:0007275; P:development; TAS.
 InterPro; IPR001323; EPO_TPO.
 InterPro; IPR003978; thrombopoietin.
 Pfam; PF00758; EPO_TPO; 1.
 PRINTS; PR01485; THROMOPTN.
 PROSITE; PS00817; EPO_TPO; 1.
 Cytokine; Glycoprotein; Hormone; Signal; Alternative splicing;
 polymorphism.
 SIGNAL 1 21 POTENTIAL.
 CHAIN 22 353 THROMBOPOIETIN.

FT DISULFID 28 172 POTENTIAL.
 FT DISULFID 50 106 POTENTIAL.
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 340 340 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 133 136 Missing (in isoform 2).
 FT VARSPLIC 160 198 Missing (in isoform 3).
 FT VARIANT 14 14 L -> P (in dbSNP:1042346).
 FT VARIANT 116 116 G -> E (in dbSNP:1126665).
 FT CONFLICT 46 46 R -> K (in REF. 8).
 FT CONFLICT 76 76 M -> MSQ (in REF. 7).
 FT CONFLICT 113 113 Q -> E (in REF. 2).
 FT CONFLICT 131 131 T -> P (in REF. 7).
 FT CONFLICT 277 277 G -> E (in REF. 8; AAB03393/AAB03394).
 FT CONFLICT 346 346 S -> C (in REF. 8; AAB03393/AAB03394).
 SQ SEQUENCE 353 AA; 37822 MW; F0AB5449B7E5526 CRC64;
 Query Match 10.5%; Score 89; DB 1; Length 353;
 Best Local Similarity 26.3%; Pred. No. 0.45;
 Matches 41; Conservative 20; Mismatches 75; Indels 20; Gaps 5;
 QY 1 APRLLCDSRVLEKAEENITTCACRHCSENENITVDTKVNFYAKRMEVGQA 60
 DB 24 APP-ACDLRVLSKLRDSVLSQCPVHPPTVLLPAVDVDFSLGEMTKQETKA 81
 QY 61 VEYVQGLALISEAVL--RQALLVNSSQWPEPLQLHVDKAVSGLSLTLLPALGAQKEA 118
 DB 82 QDLGAVTLLEGVMAARGQLGPTCLSLGLSQVRLLLGALQSL-----LGTQ--- 132
 QY 119 ISPPDAASAAPRTITADTFKRLFRVYSNFIKGLK 154
 DB 133 -LPPOG-----RTTAHKDPNAIF-SFQHLRGRVR 161

RESULT 13

MURB_PSEAE
 ID_MURB_PSEAE STANDARD; PRT; 339 AA.
 AC Q9H2M7;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE UDP-N-acetylglucosaminylglucosamine reductase (EC 1.1.1.158) (UDP-N-
 acetylmuramate dehydrogenase).
 GN MURB OR PA2977.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PAO1;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 Garber R.L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
 Brody R.L., Coulter S.N., Polger K.R., Kas A., Larbig K., Lim R.M.,
 Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
 opportunistic pathogen."
 Nature 406:959-964(2000).
 RL Nature 406:959-964(2000).
 CC -!- FUNCTION: Cell wall formation (By similarity).
 CC -!- CATALYTIC ACTIVITY: UDP-N-acetylmuramate + NADP(+) = UDP-N-
 acetyl-3-O-(1-carboxyvinyl)-D-glucosamine + NADPH.
 CC -!- COFACTOR: FAD (By similarity).
 CC -!- PATHWAY: Peptidoglycan biosynthesis.

```
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the murB family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF004723; AAG06365.1; --
CC F1R; A83274; A83274.
CC HSP; P08373; 2MER.
CC InterPro; IPR003170; MurB.
CC Pfam; PF01565; FAD binding_4; 1.
CC Oxidoreductase; NADP; Flavoprotein; FAD; Cell wall; Cell division;
CC Peptidoglycan synthesis; Complete proteome
CC SEQUENCE 339 AA; 37627 MW; C0C8EF9F2938FE27 CRC64;
CC -----
Query Match 9.8%; Score 83; DB 1; Length 339;
Best Local Similarity 22.7%; Pred. No. 1.6;
Matches 41; Conservative 22; Mismatches 48; Indels 70; Gaps 8;
QY 31 EHCSLNE-NITVPDYKYNFYANKMEVGVQAVVWQGLLSEAVLQGLLV----- 82
DB 7 EHCSLPEYNTFGIDVRALLAHARDE-----ADVREALALARE---RLPLVLVGGGSLN 58
QY 83 -----NSSQPWEP-LQLHVDKAVSGLSRLTLL 109
DB 59 LLTRDVEALVLRMASOGRIVSDAADSVLVEAEAGEANDPFWQSLERGLAGLENLSLI- 117
QY 110 RALGAQKEALSPDPAASAPLRTITIA-----DTRKLFVYSNFRKGLKLYTGEACRT 163
DB 118 -----PGTVGAAPMCNIGAYVELKDFDLSLAL--DRQDGTLEFRDQACRF 163
QY 164 G 164
DB 164 G 164
RESULT 14
CH60 BUCPP
ID CH60 BUCPP STANDARD; PRT; 548 AA.
AC Q8KTX4;
DE 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE 60 kDa chaperonin (protein Cpn60) (groEL protein).
GN GROEL OR GROEL.
OS Buchnera aphidicola (subsp. Pterocomma populeum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=99792;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22077640; PubMed=12082135;
RA Fares M.A., Barrio E., Sabater-Munoz B., Moya A.;
RT "The evolution of the heat-shock protein GroEL from Buchnera, the
RL Mol. Biol. Evol. 19:1162-1170(2002).
CC -!- FUNCTION: Prevents misfolding and promotes the refolding and
CC proper assembly of unfolded polypeptides generated under stress
CC conditions (By similarity).
CC -!- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of
CC 7 subunits (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the chaperonin (HSP60) family.
CC -----
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ439083; CAD27795.1; --
CC HAMAP; MF_006001; --; 1
CC InterPro; IPR001844; Chaprinin_Cpn60.
CC InterPro; IPR002423; Cpn60/TCP-1.
CC InterPro; IPR008950; GroEL-ATPase.
CC Pfam; PF00118; Cpn60_TCP1; 1.
CC PRINTS; PR00298; CHAPERONIN60.
CC PRINTS; PR00304; TCOMPLEXTCP1.
CC PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KW Chaperone; ATP-binding.
SQ SEQUENCE 548 AA; 57818 MW; C5C8B35D079404D CRC64;
CC -----
Query Match 9.7%; Score 82; DB 1; Length 548;
Best Local Similarity 24.3%; Pred. No. 3.6;
Matches 43; Conservative 33; Mismatches 69; Indels 32; Gaps 9;
QY 10 RVLERYLLEA-KEAENITTCGAHCNLENITV---PDTKVNFYANKME-VGQQAQV-EV 63
DB 118 RGIDKAVISAEVELKNSLVTCSKAITQVGTISANADEKVGSLIAEMEKVNDGVITV 177
QY 64 WGLLALISE-AVLRGQAL-----LVNSQPW-----EPLQLHVDKAVSGLSRLTLL 109
DB 178 EGGTGLQLELVKMGQFDRGLSPYINKSETGIVLENPYILMADKKISNIREMLPIL 237
QY 110 RALGAQKEALSPDPAASAPLRTITAD-TFRKLFVYSNFRKGLKLYTGEACRTGD 165
DB 238 ESV-----AKSGKPLLI:SEDLGEALTLVNSMRGIVKVAAPKAPGFGD 283
RESULT 15
POLG HCVJ8
ID POLG HCVJ8 STANDARD; PRT; 3033 AA.
AC P26661;
DE 01-AUG-1992 (Rel. 23, Created)
DE 01-AUG-1992 (Rel. 23, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Genome polyprotein [Contains: Capsid protein C (Core protein) (P22);
DE Envelope glycoprotein E1 (GP32) (GP35); Envelope glycoprotein E2
DE (GP68) (GP70) (NS1); Protein P7; Nonstructural protein NS2 (P21)
DE (EC 3.4.22.-); Protease/helicase NS3 (P70) (Hepacivirin)
DE NS4B (P27); Nonstructural protein NS4A (P4); Nonstructural protein
DE NS5B (P66) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].
DE Hepatitis C virus (isolate HC-J8) (HCV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11115;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92230232; PubMed=1314459;
RA Okamoto H., Kurai K., Okada S.-I., Yamamoto K., Lizuka H., Tanaka T.,
RA Fukuda S., Tsuda F., Mishiro S.;
RT "Full-length sequence of a hepatitis C virus genome having poor
RT homology to reported isolates: comparative study of four distinct
RT genotypes."
RL Virology 188:331-341(1992).
CC -!- FUNCTION: The small proteins NS2A, NS2B, NS4A and NS4B are
CC hydrophobic, suggesting a possible membrane-related function. NS3
CC and NS5 may play a role in the viral RNA replication.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the viral
CC precursor polyprotein, commonly with Asp or Glu in the P6
CC position, Cys or Thr in P1 and Ser or Ala in P1'.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC (RNA)(N).
CC -!- SUBUNIT: The virion of this virus is a nucleocapsid covered by a
CC lipoprotein envelope. The envelope consists of two proteins:
CC
```

protein M and glycoprotein E. The nucleocapsid is a complex of protein C and RNA.
-1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S29.

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EMBL; D10988; BAA01761.1; -;
PIR; A40250; GNWVJ8.
HSSP; P27958; 1HEI.
MEROPS; S29.001; -;
MEROPS; U39.001; -;
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001410; DEAD.
InterPro; IPR002522; HCV capsid.
InterPro; IPR002521; HCV core.
InterPro; IPR002519; HCV env.
InterPro; IPR002531; HCV NS1.
InterPro; IPR002518; HCV NS2.
InterPro; IPR000745; HCV NS4a.
InterPro; IPR001490; HCV NS4b.
InterPro; IPR002868; HCV NS5a.
InterPro; IPR002166; HCV RdRp.
InterPro; IPR004109; Peptidase C29.
InterPro; IPR007095; RNA_pol_DS_PS.
InterPro; IPR007094; RNA_pol_PSVir.
Pfam; PF01543; HCV capsid; 1.
Pfam; PF01542; HCV core; 1.
Pfam; PF01539; HCV env; 1.
Pfam; PF01560; HCV NS1; 1.
Pfam; PF01538; HCV NS2; 1.
Pfam; PF02907; HCV NS3; 1.
Pfam; PF01006; HCV NS4a; 1.
Pfam; PF01001; HCV NS4b; 1.
Pfam; PF01506; HCV NS5a; 1.
Pfam; PF00998; Viral RdRp; 1.
ProDom; PD186062; HCV NS1; 1.
SMART; SM00487; DEXDc1; 1.
Polyprotein; Glycoprotein; Transferase; RNA-directed RNA polymerase;
Core protein; Coat protein; Envelope protein; Helicase; ATP-binding;
Transmembrane; Nonstructural
INIT_MET 1 1
CHAIN 1 115
CHAIN 116 191
CHAIN 192 383
CHAIN 384 733
CHAIN 734 1010
CHAIN 1011 1619
CHAIN 1620 1866
CHAIN 1867 2017
CHAIN 2018 3033
CHAIN 347 369
ACT SITE 1087 1087
ACT SITE 1111 1111
ACT SITE 1169 1169
NP_BIND 1234 1241
SITE 1320 1323
SITE 1320 1323
CARBOHYD 196 196
CARBOHYD 209 209
CARBOHYD 233 233
CARBOHYD 299 299
CARBOHYD 305 305
CARBOHYD 417 417
CARBOHYD 423 423
CARBOHYD 430 430
CARBOHYD 448 448
CARBOHYD 477 477

FT CARBOHYD 534 534 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 542 542 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 558 558 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 578 578 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 649 649 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1091 1091 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2038 2038 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2359 2359 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2811 2811 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 3033 AA; 330177 MW; 1A173E7E3381FD1A CRC64;

Query Match 9.5%; Score 80.5; DB 1; Length 3033;
Best Local Similarity 26.6%; Pred. No. 39;
Matches 41; Conservative 22; Mismatches 64; Indels 27; Gaps 7;

QY 5 LIDSSVLELYLLEAKAEENITTCGAE---HCSLNENITV-PDTKVNFYAWKRM----- 54
Db 1659 IMTSSWVLGGVLAAYAVCLATGCGISIIIGRLHNDRVVAVDPDKELLVEAFDEMEECASK 1718
QY 55 ----EVGQQAENVWQG--LALLSEAVLRGQALLVNSSQWPELQ-----LHVDKAVSGLR 104
Db 1719 AALIERGQMAEMLKSKIQLLQQAQDIQATROAQDIQAIOSSWPKLSQFWAKHMMNFISGIQY 1778
QY 105 LITLLRGLG----AQKEALSPDPAASAAPLRIT 134
Db 1779 LAGLSTLPGNPAVASMAFES---AALTSPLEPTST 1809

Search completed: May 25, 2004, 11:22:05
Job time : 19 secs

GenCore version 5.1.6
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M protein - protein search, using sw model

Run on: May 25, 2004, 11:19:03 ; Search time 39 Seconds
(without alignments)
1334.885 Million cell updates/sec

Title: US-09-830-964-1

Perfect score: 846

Sequence: 1 APRRLICDSRVLYRLLKAEK.....SNFLRGKLYTGCACTGTD 165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTEMBL_25.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_todent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_virus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	723	85.5	192	Q867B1	Q867b1 equus caball
2	680.5	80.4	195	Q9GKA2	Q9gka2 oryctolagus
3	680.5	80.4	195	Q9GKA3	Q9gka3 oryctolagus
4	678	80.1	194	Q9MYM8	Q9mym8 sus scrofa
5	663	78.4	133	Q8H288	Q8h288 gorilla gor
6	658	77.8	133	Q8H289	Q8h289 pan troglod
7	627	74.1	131	Q8H287	Q8h287 pongo pygma
8	607	71.7	133	Q8H286	Q8h286 macaca sp.
9	554	65.5	133	Q8H285	Q8h285 saquinus oe
10	188	22.2	50	Q9QV40	Q9qv40 rattus sp.
11	88	10.4	323	Q8ZDC8	Q8zdc8 yersinia pe
12	87.5	10.3	346	Q8ZKZ4	Q8zkz4 salmonella
13	87.5	10.3	346	Q8ZKZ5	Q8zkz5 salmonella
14	85	10.0	3722	P94873	P94873 lysobacter
15	83	9.8	296	Q8ZAV4	Q8zav4 yersinia pe
16	82.5	9.8	154	Q87AY9	Q87ay9 xyliella fas

ALIGNMENTS

RESULT 1

Q867B1 ID Q867B1 PRELIMINARY; PRT; 192 AA.
AC Q867B1;
DT 01-JUN-2003 (TEMBLrel. 24, Created)
DT 01-JUN-2003 (TEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Erythropoietin.
GN EPO.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
CX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Kidney;
RA Sato F.;
RT "Equus caballus mRNA for erythropoietin, complete cds."
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB100030; BAC55239.1; "
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR003013; Erythropn.
DR Pfam; PF00758; EPO_TPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
SQ SEQUENCE 192 AA; 20984 MW; E02D098490B09C4F CRC64;

Query Match 85.5%; Score 723; DB 6; Length 192;
Best Local Similarity 84.8%; Pred. No. 8.4e-63;
Matches 140; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 APRRLICDSRVLYRLLKAEK...ITTCAGHCSLNENITVPDTKNFYAKMEVQQA 60

Db 27 APRRLICDSRVLYRLLKAEK...ITTCAGHCSLNENITVPDTKNFYAKMEVQQA 86

QY 61 VEWQGLALLSEAVLRGQALLVNSQPEPLQLHVDKAVSLRLTLRLALGAQKEAIS 120

Q7ZUK7 brachydanio
Q9DHD6 hepatitis c
Q9FK91 arabidopsis
Q81J9 saccharomyc
Q8DHE3 synchococcc
Q7718 hepatitis c
Q77H9 hepatitis c
Q98J10 pseudomonas
Q8UJ6 rhodospirillum
Q86808 streptomyces
Q91ZAL hepatitis c
Q7710 hepatitis c
Q43380 avena sativ
Q81713 caenorhabdi
Q81715 caenorhabdi
Q8431 mus musculu
Q8Z99 salmonella
Q80213 mus musculu
Q9529 hepatitis c
Q7712 hepatitis c
Q7717 hepatitis c
Q7716 hepatitis c
Q77H6 hepatitis c
Q77H5 hepatitis c
Q77H4 hepatitis c
Q77H3 hepatitis c
Q86751 streptomyces
Q8ZK3 pyrobaculum
Q8UB9 agrobacteri

17 82.5 9.8 558 13 Q7ZUK7
18 82.5 9.8 303 12 Q9DHD6
19 82 9.7 815 10 Q9FK91
20 81.5 9.6 436 3 Q8UJ9
21 80.5 9.5 266 16 Q8DHE3
22 80.5 9.5 303 12 Q7718
23 80.5 9.5 303 12 Q77H9
24 80 9.5 762 16 Q8J10
25 79.5 9.4 935 16 Q8UJ6
26 79.5 9.4 1829 16 Q86808
27 79.5 9.4 303 12 Q91ZAL
28 79.5 9.4 303 12 Q7710
29 79 9.3 480 10 Q43380
30 79 9.3 1250 5 Q81713
31 79 9.3 2456 5 Q81715
32 78.5 9.3 583 11 Q8431
33 78.5 9.3 813 16 Q8Z99
34 78.5 9.3 934 11 Q80213
35 78.5 9.3 3019 12 Q9529
36 78.5 9.3 303 12 Q7712
37 78.5 9.3 303 12 Q7717
38 78.5 9.3 303 12 Q7716
39 78.5 9.3 303 12 Q77H6
40 78.5 9.3 303 12 Q77H5
41 78.5 9.3 303 12 Q77H4
42 78.5 9.3 303 12 Q77H3
43 78 9.2 348 16 Q86751
44 78 9.2 378 17 Q8ZK3
45 78 9.2 455 16 Q8UB9

```

Db      87 VEVWQGLALLSEAILQOALLANSSQSPETLRHVDKAVSLASLTLRALGAQKEAIS 146
QY      121 PPDAASAAPLTIADTFKRLFRVYSNLFRLGKLYTGEACRTGD 165
Db      147 PPDAASAAPLTFVADTLCKLFRVYSNLFRLGKLYTGEACRRGD 191

RESULT 2
Q9GKA2 PRELIMINARY; PRT; 195 AA.
AC Q9GKA2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Erythropoietin.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21290682; PubMed=11396976;
RA Vilalta A., Wu D., Margalith M., Hobart P.;
RT "Rabbit EPO Gene and cDNA: Expression of Rabbit EPO after
RT Intramuscular Injection of pDNA.";
RL Biochem. Biophys. Res. Commun. 284:823-827(2001).
DR EMBL; AF290943; AAG36962.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001323; EPO_TPO.
DR Pfam; PF00758; EPO_TPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
SQ SEQUENCE 195 AA; 21025 MW; 1F1DC7F403A303EC CRC64;

Query Match 80.4%; Score 680.5; DB 6; Length 195;
Best Local Similarity 81.3%; Pred. No. 1.2e-58;
Matches 135; Conservative 12; Mismatches 18; Indels 1; Gaps 1;

QY 1 APPRLICDSRLVRLYLEAKEAENITTCGAHCSLNENITVPDTKVNFKYAKRMEVQQA 60
Db 29 APARLICDSRLVRLYLEAKEAENITTCGAHCSLNENITVPDTKVNFKYAKRMEVQQA 88

QY 61 VEVWQGLALLSEAVLRQALLVNSQFWEPLQLHVDKAVSLRSLTLRALGAQKEAIS 120
Db 89 VEVWQGLALLSEAVLRQALLVNSQFWEPLQLHVDKAVSLRSLTLRALGAQKEAIS 148

QY 121 PPDAASAAPLTIADTFKRLFRVYSNLFRLGKLYTGEACRTGD 165
Db 149 PPEAASAAPLTIADTFKRLFRVYSNLFRLGKLYTGEACRRGD 194

RESULT 3
Q9GKA3 PRELIMINARY; PRT; 195 AA.
AC Q9GKA3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Erythropoietin.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21290682; PubMed=11396976;
RA Vilalta A., Wu D., Margalith M., Hobart P.;
RT "Rabbit EPO Gene and cDNA: Expression of Rabbit EPO after
RT Intramuscular Injection of pDNA.";
RL Biochem. Biophys. Res. Commun. 284:823-827(2001).
DR EMBL; AF290943; AAG36962.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001323; EPO_TPO.
DR Pfam; PF00758; EPO_TPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
SQ SEQUENCE 195 AA; 21025 MW; 1F1DC7F403A303EC CRC64;

Query Match 80.4%; Score 680.5; DB 6; Length 195;
Best Local Similarity 81.3%; Pred. No. 1.2e-58;
Matches 135; Conservative 12; Mismatches 18; Indels 1; Gaps 1;

QY 1 APPRLICDSRLVRLYLEAKEAENITTCGAHCSLNENITVPDTKVNFKYAKRMEVQQA 60
Db 29 APARLICDSRLVRLYLEAKEAENITTCGAHCSLNENITVPDTKVNFKYAKRMEVQQA 88

QY 61 VEVWQGLALLSEAVLRQALLVNSQFWEPLQLHVDKAVSLRSLTLRALGAQKEAIS 120
Db 89 VEVWQGLALLSEAVLRQALLVNSQFWEPLQLHVDKAVSLRSLTLRALGAQKEAIS 148

QY 121 PPDAASAAPLTIADTFKRLFRVYSNLFRLGKLYTGEACRTGD 165
Db 149 PPEAASAAPLTIADTFKRLFRVYSNLFRLGKLYTGEACRRGD 194

RESULT 4
Q9MYM8 PRELIMINARY; PRT; 194 AA.
AC Q9MYM8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Erythropoietin precursor.
GN EPO.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NORWEGIAN LANDRACE; TISSUE=Kidney;
RA David B., Harbitz I.;
RT "The porcine erythropoietin gene: cDNA and genomic sequences and
RT expression analyses.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ249745; CAB96416.1; -.
DR EMBL; AJ249746; CAB96417.1; -.
DR HSSP; P01588; 1CN4.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001323; EPO_TPO.
DR Pfam; PF00758; EPO_TPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 194 AA; 21303 MW; 77881A6F6F20EA1C CRC64;

Query Match 80.1%; Score 678; DB 6; Length 194;
Best Local Similarity 82.0%; Pred. No. 2.2e-58;
Matches 137; Conservative 7; Mismatches 21; Indels 2; Gaps 1;

QY 1 APPRLICDSRLVRLYLEAKEAENITTCGAHCSLNENITVPDTKVNFKYAKRMEVQQA 60

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RT Intramuscular Injection of pDNA.";
RL Biochem. Biophys. Res. Commun. 284:823-827(2001).
DR EMBL; AF290943; AAG36961.1; -.
DR PIR; JC7699; JC7699.
DR HSSP; P01588; 1CN4.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR003013; Erythropn.
DR Pfam; PF00758; EPO_TPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
SQ SEQUENCE 195 AA; 21053 MW; 0999DA7D852713F3 CRC64;

Query Match 80.4%; Score 680.5; DB 6; Length 195;
Best Local Similarity 81.3%; Pred. No. 1.2e-58;
Matches 135; Conservative 12; Mismatches 18; Indels 1; Gaps 1;

QY 1 APPRLICDSRLVRLYLEAKEAENITTCGAHCSLNENITVPDTKVNFKYAKRMEVQQA 60
Db 29 APARLICDSRLVRLYLEAKEAENITTCGAHCSLNENITVPDTKVNFKYAKRMEVQQA 88

QY 61 VEVWQGLALLSEAVLRQALLVNSQFWEPLQLHVDKAVSLRSLTLRALGAQKEAIS 120
Db 89 VEVWQGLALLSEAVLRQALLVNSQFWEPLQLHVDKAVSLRSLTLRALGAQKEAIS 148

QY 121 PPDAASAAPLTIADTFKRLFRVYSNLFRLGKLYTGEACRTGD 165
Db 149 PPEAASAAPLTIADTFKRLFRVYSNLFRLGKLYTGEACRRGD 194

RESULT 4
Q9MYM8 PRELIMINARY; PRT; 194 AA.
AC Q9MYM8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Erythropoietin precursor.
GN EPO.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NORWEGIAN LANDRACE; TISSUE=Kidney;
RA David B., Harbitz I.;
RT "The porcine erythropoietin gene: cDNA and genomic sequences and
RT expression analyses.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ249745; CAB96416.1; -.
DR EMBL; AJ249746; CAB96417.1; -.
DR HSSP; P01588; 1CN4.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001323; EPO_TPO.
DR Pfam; PF00758; EPO_TPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 194 AA; 21303 MW; 77881A6F6F20EA1C CRC64;

Query Match 80.1%; Score 678; DB 6; Length 194;
Best Local Similarity 82.0%; Pred. No. 2.2e-58;
Matches 137; Conservative 7; Mismatches 21; Indels 2; Gaps 1;

QY 1 APPRLICDSRLVRLYLEAKEAENITTCGAHCSLNENITVPDTKVNFKYAKRMEVQQA 60

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b 27 APRRLCDISVLEKEGENATMGCAESSENITVPTKVFYAKRMEVQQA 86
y 61 VEVQGLALSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRSLTLRALGAQKEAIS 120
b 87 VEVQGLALSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRSLTLRALGAQKEAIS 146
y 121 PPDA--ASAPHSITADTFKRLFRYSNPLRCKLKYTGACRTGD 165
b 147 LPDASPSSATPLRTFAVDTLCKLFRYSNPLRCKLKYTGACRRRD 193

RESULT 5
QH288 PRELIMINARY; PRT; 133 AA.
ID QH288
AC QH288;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Erythropoietin (Fragment).
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Huigin C., Tichy H., Klein J.;
RT "Molecular evolution in higher primates; gene specific and organism
specific characteristics.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY092016; AA076633.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR001323; Erythroptn.
DR Pfam; PF00758; EPO_TPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
FT NON TER 1
FT NON TER 133
SQ SEQUENCE 133 AA; 14696 MW; E2D0130942693140 CRC64;

Query Match 78.4%; Score 663; DB 6; Length 133;
Best Local Similarity 99.2%; Pred. No. 4e-57;
Matches 132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

y 9 SRVLYRLLEAKAEENITTCGAHCSLNENITVPTKVFYAKRMEVQQA 68
b 1 SRVLYRLLEAKAEENITTCGAHCSLNENITVPTKVFYAKRMEVQQA 60
y 69 LLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRSLTLRALGAQKEAIS 128
b 61 LLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRSLTLRALGAQKEAIS 120
y 129 PLRTITADTFKRL 141
b 121 PLRTITADTFKRL 133

RESULT 6
QH289 PRELIMINARY; PRT; 133 AA.
ID QH289
AC QH289;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Erythropoietin (Fragment).
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Huigin C., Tichy H., Klein J.;
RT "Molecular evolution in higher primates; gene specific and organism
specific characteristics.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY092017; AA076634.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR001323; Erythroptn.
DR Pfam; PF00758; EPO_TPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
FT NON TER 1
FT NON TER 133
SQ SEQUENCE 133 AA; 14403 MW; 143F5E4931EA03FA CRC64;

Query Match 74.1%; Score 627; DB 6; Length 131;
Best Local Similarity 95.5%; Pred. No. 1.3e-53;
Matches 126; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

y 9 SRVLYRLLEAKAEENITTCGAHCSLNENITVPTKVFYAKRMEVQQA 68
b 1 SRVLYRLLEAKAEENITTCGAHCSLNENITVPTKVFYAKRMEVQQA 58
y 69 LLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRSLTLRALGAQKEAIS 128
b 61 LLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRSLTLRALGAQKEAIS 120
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RA O'Huigin C., Tichy H., Klein J.;
RT "Molecular evolution in higher primates; gene specific and organism
specific characteristics.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY092015; AA076632.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR001323; Erythroptn.
DR Pfam; PF00758; EPO_TPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
FT NON TER 1
FT NON TER 133
SQ SEQUENCE 133 AA; 14523 MW; ECDP5609596390EB CRC64;

Query Match 77.8%; Score 658; DB 6; Length 133;
Best Local Similarity 99.2%; Pred. No. 1.2e-56;
Matches 132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

y 9 SRVLYRLLEAKAEENITTCGAHCSLNENITVPTKVFYAKRMEVQQA 68
b 1 SRVLYRLLEAKAEENITTCGAHCSLNENITVPTKVFYAKRMEVQQA 60
y 69 LLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRSLTLRALGAQKEAIS 128
b 61 LLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRSLTLRALGAQKEAIS 120
y 129 PLRTITADTFKRL 141
b 121 PLRTITADTFKRL 133

RESULT 7
QH287 PRELIMINARY; PRT; 131 AA.
ID QH287
AC QH287;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Erythropoietin (Fragment).
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Huigin C., Tichy H., Klein J.;
RT "Molecular evolution in higher primates; gene specific and organism
specific characteristics.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY092017; AA076634.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR001323; Erythroptn.
DR Pfam; PF00758; EPO_TPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
FT NON TER 1
FT NON TER 131
SQ SEQUENCE 131 AA; 14403 MW; 143F5E4931EA03FA CRC64;

Query Match 74.1%; Score 627; DB 6; Length 131;
Best Local Similarity 95.5%; Pred. No. 1.3e-53;
Matches 126; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

y 9 SRVLYRLLEAKAEENITTCGAHCSLNENITVPTKVFYAKRMEVQQA 68
b 1 SRVLYRLLEAKAEENITTCGAHCSLNENITVPTKVFYAKRMEVQQA 58
y 69 LLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRSLTLRALGAQKEAIS 128
b 61 LLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRSLTLRALGAQKEAIS 120
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Db 59 LLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAKQKASPPDAALAA 118

Qy 129 PLRTITADTFK 140

Db 119 PLRTITADTFK 130

RESULT 8

Q8H286 PRELIMINARY; PRT; 133 AA.

AC Q8H286; Score 607; DB 6; Length 133;

DT 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Erythropoietin (Fragment).

OS Macaca sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecoidea; Macaca.

OX NCBI_TaxID=9549;

RN [1]

RP SEQUENCE FROM N.A.

RA O'huigin C., Tichy H., Klein J.;

RT "Molecular evolution in higher primates; gene specific and organism

RT specific characteristics."

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY092018; AAM76635.1; -

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.

DR GO; GO:0005179; F:hormone activity; IEA.

DR InterPro; IPR001323; EPO_TPO.

DR InterPro; IPR003013; Erythroptn.

DR Pfam; PF00758; EPO_TPO; 1.

DR PRINTS; PR00272; ERYTHROPTN.

FT NON_TER 1

FT NON_TER 133

SQ SEQUENCE 133 AA; 14506 MW; 55CB11A2DC8354A0 CRC64;

Query Match 71.7%; Score 607; DB 6; Length 133;

Best Local Similarity 90.2%; Pred. No. 1.2e-51;

Matches 120; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 9 SRVLYRYLLEAKAEENITTCGAHCSSLNENITVPTDKNFYAKRMVEVQQAVVWQGLA 68

Db 1 SRVLYRYLLEAKAEENITTCGAHCSSLNENITVPTDKNFYAKRMVEVQQAVVWQGLA 60

Qy 69 LLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAKQKASPPDAASAA 128

Db 61 LLSEAVLRGQAVLNSQPWFPLQLHMDKASGLSLTLLRALGAKQKASPPDAASAA 120

Qy 129 PLRTITADTFK 141

Db 121 PLRTITADTFK 133

RESULT 9

Q8H285 PRELIMINARY; PRT; 133 AA.

AC Q8H285; Score 607; DB 6; Length 133;

DT 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Erythropoietin (Fragment).

OS Saguinus oedipus (Cotton-top tamarin).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.

OX NCBI_TaxID=9490;

RN [1]

RP SEQUENCE FROM N.A.

RA O'huigin C., Tichy H., Klein J.;

RT "Molecular evolution in higher primates; gene specific and organism

RT specific characteristics."

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY092019; AAM76636.1; -

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.

DR GO; GO:0005179; F:hormone activity; IEA.

DR InterPro; IPR001323; EPO_TPO.

DR InterPro; IPR003013; Erythroptn.

DR Pfam; PF00758; EPO_TPO; 1.

DR PRINTS; PR00272; ERYTHROPTN.

FT NON_TER 1

FT NON_TER 133

SQ SEQUENCE 133 AA; 14375 MW; C923E859BB608FEC CRC64;

Query Match 65.5%; Score 554; DB 6; Length 133;

Best Local Similarity 84.3%; Pred. No. 1.9e-46;

Matches 113; Conservative 8; Mismatches 11; Indels 2; Gaps 2;

Qy 9 SRVLYRYLLEAKAEENITTCGAHCSSLNENITVPTDKNFYAKRMVEVQQAVVWQGLA 68

Db 1 SGVLYRYVLEGEAKAEENITTCGAHCSSLNENITVPTDKNFYAKRMVEVQQAVVWQGLT 60

Qy 69 LLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAKQKASPPDAASAA 127

Db 61 LLSEAVLRGQALLVNSQPWEPLQLHMDKASGLSLTLLRALGAKQKASPPDAASAA 119

Qy 128 APLRTITADTFK 141

Db 120 VPLQITADTFK 133

RESULT 10

Q9QV40 PRELIMINARY; PRT; 50 AA.

AC Q9QV40; Score 50; DB 6; Length 50;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Erythropoietin (Fragment).

OS Rattus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI_TaxID=10118;

RN [1]

RP SEQUENCE.

RX MEDLINE=94115047; PubMed=7764337;

RA Okano M., Suga H., Masuda S., Nagao M., Narita H., Ikura K.,

RA Sasaki R.;

RL Biosci. Biotechnol. Biochem. 57:1882-1885(1993).

DR HSP; P01588; 1EER.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.

DR GO; GO:0005179; F:hormone activity; IEA.

DR InterPro; IPR001323; EPO_TPO.

DR InterPro; IPR003013; Erythroptn.

DR Pfam; PF00758; EPO_TPO; 1.

DR PRINTS; PR00272; ERYTHROPTN.

SQ SEQUENCE 50 AA; 5587 MW; 70B44A8BFE016034 CRC64;

Query Match 22.2%; Score 188; DB 11; Length 50;

Best Local Similarity 78.0%; Pred. No. 4.2e-11;

Matches 39; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 APRPLICDSRVLYRYLLEAKAEENITTCGAHCSSLNENITVPTDKNFY 50

Db 1 APRPLIXDSRVLYRYLLEAKAEENITTCGAHCSSLNENITVPTDKNFY 50

RESULT 11

Q8ZDC8 PRELIMINARY; PRT; 323 AA.

AC Q8ZDC8; Score 323; DB 6; Length 323;

DT 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

Ribonucleoside-diphosphate reductase 2 beta chain (EC 1.17.4.1).
NRDF OR YP02648 OR Y1222.
S Yersinia pestis.
C Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
C Enterobacteriaceae; Yersinia.
X NCBI_TaxID=632;
[1]
P SEQUENCE FROM N.A.
C STRAIN=CO-92 / Biovar Orientalis;
X MEDLINE=21470413; PubMed=11586360;
A Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prenice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Genome sequence of Yersinia pestis, the causative agent of plague.";
T Nature 413:523-527(2001).
L [2]
N SEQUENCE FROM N.A.
P STRAIN=KIMS / Biovar Mediaevalis;
C MEDLINE=22137863; PubMed=12142430;
X Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
Perry R.D.;
"Genome sequence of Yersinia pestis KIM.";
T J. Bacteriol. 184:4601-4611(2002).
L EMBL; AJ414153; CAC92889.1; -
R EMBL; AE013726; AM84798.1; -
R F1; AB0323; AB0323.
R GO; GO:0016491; F:oxidoreductase activity; IEA.
R GO; GO:0004748; F:ribonucleoside-diphosphate reductase activity; IEA.
R GO; GO:0009186; P:deoxyribonucleoside diphosphate metabolism; IEA.
R InterPro; IPR000358; RibonucL reductase.
R Pfam; PF00268; ribonuc red sm; 1.
R PROSITE; PS00368; RIBOED SMALL; 1.
R Oxidoreductase; Complete Proteome
X SEQUENCE 323 AA; 36823 MW; 87C21F7BBB9B7FD2 CRG64;
Query Match 10.4%; Score 88; DB 16; Length 323;
Best Local Similarity 25.2%; Pred. No. 2.8;
Matches 34; Conservative 20; Mismatches 59; Indels 22; Gaps 5;
Y 38 NITVPDTKYNFYAKRMEVQQAWEVWQGLALLSEAVLQGLVNSSQPWEPLQLHVD- 96
b 2 NVVKPITRISAINWNKIE-DKOLEVWN--RLTSNFWLPKVPKPLNDIPSWATLTPHEQQ 58
Y 97 ---KAVSLRSLTLRLALGQA---KEAISPDPDAAAPLRTITADTFKLFVYSNFLR 150
b 59 LTRVFTGLTLDITQNTLGPALIKDAITPHEAIFSNISFMEAVHARSYSSIFSTL-- 116
Y 151 GKILYTGACRTGD 165
b 117 -----CLTSD 121
RESULT 12
Q8ZKZ4
ID Q8ZKZ4 PRELIMINARY; PRT; 346 AA.
AC Q8ZKZ4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Periplasmic sensor in multi-component regulatory system with Tors
DE (sensory kinase) and Tors (Regulator), regulates tor operon.
EN TORS OR STM3825.
CS Salmonella typhimurium.
CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
CC Enterobacteriaceae; Salmonella.
CX NCBI_TaxID=602;

SEQUENCE FROM N.A.
RP STRAIN=LT2 / SGSC1412 / ATCC 700720;
RC MEDLINE=21534948; PubMed=11677609;
RX McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
L72.";
RL Nature 413:852-856(2001).
DR EMBL; AE008878; AAL22684.1; -
DR InterPro; IPR001761; PeriplaBP/LacI.
DR Pfam; PF00332; Peripla_BP_like; 1.
KW Complete proteome.
SQ SEQUENCE 346 AA; 38440 MW; E37CAB58E49FD716 CRC64;
Query Match 10.3%; Score 87.5; DB 16; Length 346;
Best Local Similarity 26.7%; Pred. No. 3.4;
Matches 44; Conservative 22; Mismatches 48; Indels 51; Gaps 9;
Y 10 RVLYRYLLEAKAEENITG--CAEHCSLNE--NITVPDTKYNFYAKRMEVQQAWEVWQ 65
b 217 RNLQEMLERHPDANVAGSATAAAMGEGRNLTPTLTIVSYFL-----THQVYR 267
Y 66 GLALLSEAVLQGLVNSSQ-PWEPLQLHVDKAVSGLSLTLRLALGQA--KEAISP 122
b 268 GLK-----RGHILMAUSDQAWQ-----GELAITQSIKVLQGPVFNISPP 309
Y 123 -----DAASAAPLRTITADTFKLFVYSNFLRGLKLYTGEA 160
b 310 VLTLTNNADSRVRSLSPPGFRPVY-----LYQYTSEA 344
RESULT 13
Q8Z2M5
ID Q8Z2M5 PRELIMINARY; PRT; 346 AA.
AC Q8Z2M5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Solute binding receptor protein.
GN STY3952 OR TORT OR T3693.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Conerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodyanni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).
DR EMBL; AL627280; CAD03169.1; -

Best Local Similarity 24.2%; Pred. No. 7.8;
Matches 48; Conservative 34; Mismatches 62; Indels 54; Gaps 10;

6 ICDSRVLERYLLLEAK-EAENITTCGAHCHSLNENIT-VPDTKVNFYAWKKEVGGQAVSV 63
32 LCDADITKVOILTAEINABSLVDNA--ASLDALITMLPENSE-----AVEQVLLGSDGISG 85
64 WQGLALLSEAVLRGOALLVNSQF-----WE-----PLQLHVDKAVSG----- 101
86 W--VAQLSQAAV--VIDMSSDPERSRRLAILLAVWELDYLDAPVSGGVKKKAQNGTILSI 140
102 -----LRSLLTLRALGAQKEAISPDAASAAP-----LRTITADTFRKLP 142
141 LIGGEDRVLKSCYTALAAMGEQILFVGPAGSGHAAKALANNVVSATGLLATIEALHVAQRF 200
143 RVYSNFRGKLYTGEA 160
201 GIEPEVMTVINTSTGRS 218

earch completed: May 25, 2004, 11:23:00
ob time : 43 secs

M protein - protein search, using sw model

run on: May 25, 2004, 11:19:33 ; Search time 20 seconds
(without alignments)
793.580 Million cell updates/sec

title: US-09-830-964-1

perfect score: 846

sequence: 1 APPRLICDSRVLYLEAK.....SNFLRGKLYTGEACRTGD 165

coring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 283366 seqs, 96191526 residues

total number of hits satisfying chosen parameters: 283366

minimum DB seq length: 0

maximum DB seq length: 200000000

post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

database :

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	846	100.0	193	1 ZUHU	erythropoietin pre
2	764.5	90.4	192	1 JQ0173	erythropoietin pre
3	759.5	89.8	192	1 I84613	erythropoietin pre
4	713	84.3	188	1 I46083	erythropoietin pre
5	701	82.9	192	1 S28148	erythropoietin pre
6	685.5	81.0	194	1 I46401	erythropoietin pre
7	681	80.5	192	1 A24302	erythropoietin pre
8	680.5	80.4	195	2 J7C789	erythropoietin - r
9	678	80.1	190	2 I46578	erythropoietin - p
10	638	75.4	175	2 I46199	erythropoietin - d
11	90	10.6	353	2 G02729	thrombopoietin - h
12	89	10.5	353	2 I80105	thrombopoietin pre
13	88	10.4	323	2 AB0323	ribonucleoside-dip
14	87.5	10.3	346	2 AE0359	Solute binding rec
15	86	10.2	286	2 A55330	megakaryocyte grow
16	83	9.8	296	2 A10443	probable 2-hydroxy
17	83	9.8	339	2 AB3274	UDP-N-acetylpyruvo
18	80.5	9.5	3033	1 GNWVJ8	genome polyprotein
19	79.5	9.4	1829	2 T35681	probable sensory h
20	79	9.3	480	2 S56639	ribosomal protein
21	78.5	9.3	813	2 AF0526	ATP-dependent heli
22	78.5	9.3	897	2 A54896	EGF receptor subst
23	78	9.2	348	2 T35450	ABC transporter Ar
24	78	9.2	455	2 AG2919	conserved hypotet
25	78	9.2	455	2 H97693	methylamine utiliz
26	78	9.2	747	1 S36741	probable copper-tr
27	77.5	9.2	242	2 AD1928	hypothetical prote
28	77	9.1	451	2 S75569	hypothetical prote
29	76.5	9.0	154	2 H82810	bacterioferritin X

RESULT 1

ZUHU

erythropoietin precursor [validated] - human

C/Species: Homo sapiens (man)

C/Date: 27-Nov-1985 #sequence, revision 27-Nov-1985 #text_change 08-Dec-2000

C/Accession: A01855; A24744; A25384; A22210; S56178

R/Jacobs, K.; Shoemaker, C.; Rudersdorf, R.; Neill, S.D.; Kaufman, R.J.; Mufson, A.; Seel

Nature 313, 806-810, 1985

A/Title: Isolation and characterization of genomic and cDNA clones of human erythropoiet

A/Reference number: A01855; MUID:85137899; PMID:3838366

A/Accession: A01855

A/Molecule type: mRNA; DNA

A/Residues: 1-193 <JAC>

R/Lin, F.K.; Sugars, S.; Lin, C.H.; Browne, J.K.; Smalling, R.; Egrie, J.C.; Chen, K.K.; I

Proc. Natl. Acad. Sci. U.S.A. 82, 7580-7584, 1985

A/Title: Cloning and expression of the human erythropoietin gene.

A/Reference number: A24744; MUID:86067948; PMID:3865178

A/Accession: A24744

A/Molecule type: DNA

A/Residues: 1-193 <LIN>

A/Cross-references: GB:M13119; NID:g182197; PIDN:AAA52400.1; PID:g182198

R/Lai, P.H.; Everett, R.; Wang, F.F.; Arakawa, T.; Goldwasser, E.

J. Biol. Chem. 261, 3116-3121, 1986

A/Title: Structural characterization of human erythropoietin.

A/Reference number: A25384; MUID:86140080; PMID:3949763

A/Accession: A25384

A/Molecule type: protein

A/Residues: 28-86, 'Q', 87-193 <LAI>

A/Experimental source: urine

A/Note: forms without the carboxyl-terminal residue and the four carboxyl-terminal resid

R/Yanagawa, S.; Hirade, K.; Ohnaka, H.; Sasaki, R.; Chiba, H.; Ueda, M.; Goto, M.

J. Biol. Chem. 259, 2707-2710, 1984

A/Title: Isolation of human erythropoietin with monoclonal antibodies.

A/Reference number: A22210; MUID:84135751; PMID:6698989

A/Accession: A22210

A/Molecule type: protein

A/Residues: 28-29, 'X', 31-33, 'L', 35-50, 'X', 52-53, 'D', 55, 'G', 57 <YAN>

R/Matsumoto, S.; Ikura, K.; Ueda, M.; Sasaki, R.

Plant Mol. Biol. 27, 1163-1172, 1995

A/Title: Characterization of a human glycoprotein (erythropoietin) produced in cultured

A/Reference number: S56178; MUID:95284365; PMID:7766897

A/Accession: S56178

A/Molecule type: protein

A/Residues: 28-33, 'X', 35-37 <WTS>

C/Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o

C/Genetics:

A/Gene: GDB:EPO

A/Cross-references: GDB:i119110; OMIM:133170

A/Map position: 7q21.3-7q22.1

A/Introns: 5/1, 53/3, 82/3, 142/3

C/Function:

```
A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-193/Product: erythropoietin #status experimental
F;34-188,56-60/Disulfide bonds: #status experimental
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;153/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 100.0%; Score 846; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e-74; Indels 0; Gaps 0;
Matches 165; Conservative 0; Mismatches 0;

QY 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 60
Db 28 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 87

QY 61 VEVWQGLALLSEAVLRGQALLVNSQPEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
Db 88 VEVWQGLALLSEAVLRGQALLVNSQPEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 147

QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGD 165
Db 148 PPDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGD 192

RESULT 2
JQ0173
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 07-SEP-1990 #sequence_revision 15-Nov-1996 #text_change 22-Jun-1999
C;Accession: JQ0173
R;Lin, F.K.; Lin, C.H.; Lai, P.H.; Browne, J.K.; Egrie, J.C.; Smalling, R.; Fox, G.M.;
Gene 44, 201-209, 1986
A;Title: Monkey erythropoietin gene: cloning, expression and comparison with the human e
A;Reference number: JQ0173; MUID:87055236; PMID:2877922
A;Accession: JQ0173
A;Molecule type: mRNA
A;Residues: 1-192 <LIN>
A;Cross-references: GB:M18189; GB:M18188; GB:M18189; GB:M18188; NID:G342093; PIDN:AAA368
A;Experimental source: kidney
C;Comment: This protein is the principal hormone involved in the regulation of erythrocy
C;Function: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-192/Product: erythropoietin #status predicted <MAT>
F;34-187,56-60/Disulfide bonds: #status predicted
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 90.4%; Score 764.5; DB 1; Length 192;
Best Local Similarity 91.5%; Pred. No. 1.7e-66; Indels 1; Gaps 1;
Matches 151; Conservative 7; Mismatches 6;

QY 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 60
Db 28 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 87

QY 61 VEVWQGLALLSEAVLRGQALLVNSQPEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
Db 88 VEVWQGLALLSEAVLRGQALLVNSQPEPLQLHVDKAVSGLSRLTLLRALGAQ-EAIS 146

QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGD 165
Db 147 LPDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGD 191

RESULT 3
I84613
erythropoietin precursor - rhesus macaque

A;Species: Macaca mulatta (rhesus macaque)
C;Date: 02-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 22-Jun-1999
C;Accession: I84613
R;Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A;Title: Erythropoietin structure-function relationships: High degree of sequence homolo
A;Reference number: I46083; MUID:93372347; PMID:8364201
A;Accession: I84613
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-192 <RES>
A;Cross-references: GB:L10609; NID:G342095; PIDN:AAA36842.1; PID:G342096
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
C;Function: the primary inducer of erythrocyte formation
A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-192/Product: erythropoietin #status predicted <MAT>
F;34-187,56-60/Disulfide bonds: #status predicted
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 89.8%; Score 759.5; DB 1; Length 192;
Best Local Similarity 90.3%; Pred. No. 5.1e-66; Indels 1; Gaps 1;
Matches 149; Conservative 9; Mismatches 6;

QY 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 60
Db 28 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 87

QY 61 VEVWQGLALLSEAVLRGQALLVNSQPEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
Db 88 VEVWQGLALLSEAVLRGQALLVNSQPEPLQLHVDKAVSGLSRLTLLRALGAQ-EAIS 146

QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGD 165
Db 147 LPDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGD 191

RESULT 4
I46083
erythropoietin precursor - cat (fragment)
C;Species: Felis silvestris catus (domestic cat)
C;Date: 16-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 22-Jun-1999
C;Accession: I46083
R;Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A;Title: Erythropoietin structure-function relationships: High degree of sequence homolo
A;Reference number: I46083; MUID:93372347; PMID:8364201
A;Accession: I46083
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-188 <WEN>
A;Cross-references: GB:L10606; NID:G163820; PIDN:AAA30807.1; PID:G163821
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
C;Function: the primary inducer of erythrocyte formation
A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F;23-188/Product: erythropoietin #status predicted <MAT>
F;29-183,51-55/Disulfide bonds: #status predicted
F;46,60,105/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;148/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 84.3%; Score 713; DB 1; Length 188;
Best Local Similarity 84.2%; Pred. No. 1.6e-61; Indels 0; Gaps 0;
Matches 139; Conservative 9; Mismatches 17;

QY 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 60
Db 23 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 82
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A;Residues: 1-194 <FUD>
A;Cross-references: EMBL:Z24681; NID:g395049; PIDN:CAA80848.1; PID:g395050
R;Wen, D.; Boisssel, J.
Blood 82, 1507-1516, 1993
A;Title: Erythropoietin structure-function relationships: High degree of sequence homology
A;Reference number: I46083; MUID:93372347; PMID:8364201
A;Accession: I47077
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 4-15, 'L', 17-107, 'P', 109-194 <WEN>
A;Cross-references: GB:I10610; NID:g165876; PIDN:AAA31518.1; PID:g165877
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
C;Function:
A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-194/Product: erythropoietin #status predicted <MAT>
F;34-189,56-60/Disulfide bonds: #status predicted
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;154/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 81.0%; Score 685.5; DB 1; Length 194;
Best Local Similarity 81.9%; Pred. No. 7.4e-59;
Matches 136; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

Qy 1 APPRLICDSRVLELYLLEAKAEENITTCAGHCSLNENITVPTKKNFYAKRWMEVQQA 60
Db 28 APPRLICDSRVLELYLLEAKAEENITTCAGHCSLNENITVPTKKNFYAKRWMEVQQA 87
Qy 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120
Db 88 LEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIP 147
Qy 121 PPDAASAPLRITADTFKLFVYSNLFRLGKLYTGEACRTGD 165
Db 148 LPDATPSAAPLRITADTFKLFVYSNLFRLGKLYTGEACRTGD 193
RESULT 7
A24902
A;Title: Erythropoietin precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 25-Oct-1987 #sequence_revision 15-Nov-1996 #text_change 22-Jun-1999
C;Accession: A24902; A24901
R;Shoemaker, C.B.; Mitsock, L.D.
Mol. Cell. Biol. 6, 849-858, 1986
A;Title: Murine erythropoietin gene: cloning, expression, and human gene homology.
A;Reference number: A24902; MUID:87039105; PMID:3773894
A;Accession: A24902
A;Molecule type: DNA
A;Residues: 1-192 <SHO>
A;Note: the authors translated the codon TTA for residue 12 as Phe, TTA for residue 43 a
R;McDonald, J.D.; Lin, F.K.; Goldwasser, E.
Mol. Cell. Biol. 6, 842-848, 1986
A;Title: Cloning, sequencing, and evolutionary analysis of the mouse erythropoietin gene
A;Reference number: A24901; MUID:87039104; PMID:3022133
A;Accession: A24901
A;Molecule type: DNA
A;Residues: 1-67, 'P', 69-192 <MCD>
A;Cross-references: GB:M12930; NID:g193086; PIDN:AAA37570.1; PID:g387152
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver
C;Genetics:
A;Introns: 5/1; 52/3; 81/3; 141/3
C;Function:
A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-192/Product: erythropoietin #status predicted <MAT>
F;33-187,55-165/Disulfide bonds: #status predicted
F;50,64,109/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 82.9%; Score 701; DB 1; Length 192;
Best Local Similarity 82.4%; Pred. No. 2.3e-60;
Matches 136; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

Qy 1 APPRLICDSRVLELYLLEAKAEENITTCAGHCSLNENITVPTKKNFYAKRWMEVQQA 60
Db 27 APPRLICDSRVLELYLLEAKAEENITTCAGHCSLNENITVPTKKNFYAKRWMEVQQA 86
Qy 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120
Db 87 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 146
Qy 121 PPDAASAPLRITADTFKLFVYSNLFRLGKLYTGEACRTGD 165
Db 147 PPDAQAPLRITADTFKLFVYSNLFRLGKLYTGEACRTGD 191
RESULT 6
I46401
A;Title: Erythropoietin precursor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 16-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 22-Jun-1999
C;Accession: I46401; I47077
R;Fu, P.; Evans, B.; Lim, G.B.; Moritz, K.; Wintour, E.M.
Mol. Cell. Endocrinol. 93, 107-116, 1993
A;Title: The sheep erythropoietin gene: molecular cloning and effect of hemorrhage on pl
A;Reference number: I46401; MUID:93351736; PMID:8349021
A;Accession: I46401
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA

Query Match 80.5%; Score 681; DB 1; Length 192;
Best Local Similarity 79.4%; Pred. No. 2e-58;
Matches 131; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVQQA 60
DB 27 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVQQA 86

QY 61 VEVWQGLALLSEAVLRGQALLVNSQSPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120
DB 87 VEVWQGLALLSEAVLRGQALLVNSQSPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 146

QY 121 PPDAASAAPLRTITADTFPKLFRVYSNFRGKGLKLYTGEACRTGD 165
DB 147 PPDTPPAPLRTITADTFPKLFRVYSNFRGKGLKLYTGEACRTGD 191

RESULT 8
JC7699
erythropoietin - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
C:Accession: JC7699
R:Vitalba, A.; Wu, D.; Margalith, M.; Hobart, P.
Biochem. Biophys. Res. Commun. 284, 823-827, 2001
A:Title: Rabbit EPO gene and cDNA: Expression of rabbit EPO after intramuscular injection
A:Reference number: JC7699; MUID:21290682; PMID:11396976
A:Contents: Kidney
A:Accession: JC7699
A:Molecule type: DNA
A:Residues: 1-195 <VIL>
A:Cross-references: GB:AF290943
C:Comment: This protein, a heavily glycosylated 34K protein produced in the fetal liver
cytes.
C:Genetics:
A:Gene: epo
C:Superfamily: erythropoietin
C:Keywords: glycoprotein; kidney

Query Match 80.4%; Score 680.5; DB 2; Length 195;
Best Local Similarity 81.3%; Pred. No. 2.3e-58;
Matches 135; Conservative 12; Mismatches 18; Indels 1; Gaps 1;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVQQA 60
DB 29 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVQQA 88

QY 61 VEVWQGLALLSEAVLRGQALLVNSQSPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120
DB 89 VEVWQGLALLSEAVLRGQALLVNSQSPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 148

QY 121 PPDAASAAPLRTITADTFPKLFRVYSNFRGKGLKLYTGEACRTGD 165
DB 149 PPDASAAPLRTITADTFPKLFRVYSNFRGKGLKLYTGEACRTGD 194

RESULT 9
I46578
erythropoietin - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
C:Accession: I46578
R:Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A:Title: Erythropoietin structure-function relationships: High degree of sequence homology
A:Reference number: I46083; MUID:93372347; PMID:8364201
A:Accession: I46578
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-190 <WEN>
A:Cross-references: GB:I10607; NID:g164445; PIDN:AAA31029.1; PID:g164446
C:Superfamily: erythropoietin

Query Match 80.1%; Score 678; DB 2; Length 190;
Best Local Similarity 82.0%; Pred. No. 3.8e-58;
Matches 137; Conservative 7; Mismatches 21; Indels 2; Gaps 1;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVQQA 60
DB 23 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVQQA 82

QY 61 VEVWQGLALLSEAVLRGQALLVNSQSPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120
DB 83 VEVWQGLALLSEAVLRGQALLVNSQSPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 142

QY 121 PPDAASAAPLRTITADTFPKLFRVYSNFRGKGLKLYTGEACRTGD 165
DB 143 LPDASPSSAPLRTITADTFPKLFRVYSNFRGKGLKLYTGEACRTGD 189

RESULT 10
I46199
erythropoietin - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 23-Jul-1999
C:Accession: I46199
R:Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A:Title: Erythropoietin structure-function relationships: High degree of sequence homology
A:Reference number: I46083; MUID:93372347; PMID:8364201
A:Accession: I46199
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-175 <WEN>
A:Cross-references: GB:I13027; NID:g290087; PIDN:AAA30842.1; PID:g552347
C:Superfamily: erythropoietin

Query Match 75.4%; Score 638; DB 2; Length 175;
Best Local Similarity 81.0%; Pred. No. 2.6e-54;
Matches 124; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVQQA 60
DB 23 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVQQA 82

QY 61 VEVWQGLALLSEAVLRGQALLVNSQSPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 120
DB 83 VEVWQGLALLSEAVLRGQALLVNSQSPWEPLQLHVDKAVSGLSLTLRLALGAQKEAIS 142

QY 121 PPDAASAAPLRTITADTFPKLFRVYSNFRGKGL 153
DB 143 LPEASAPLRTITADTFPKLFRVYSNFRGKGL 175

RESULT 11
G02729
thrombopoietin - human
C:Species: Homo sapiens (man)
C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C:Accession: G02729
R:Im, S.
submitted to the EMBL Data Library, May 1996
A:Reference number: H01637
A:Accession: G02729
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-353 <IMX>
A:Cross-references: EMBL:U59493; NID:g1401245; PIDN:AA03392.1; PID:g1401246
C:Genetics:
A:Gene: HPO

Query Match 10.6%; Score 90; DB 2; Length 353;
Best Local Similarity 26.3%; Pred. No. 0.61;
Matches 41; Conservative 20; Mismatches 75; Indels 20; Gaps 5;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVQQA 60

Query Match 10.5%; Score 89; DB 2; Length 353;
Best Local Similarity 26.3%; Pred. No. 0.76; Mismatches 20; Indels 20; Gaps 5;
Matches 41; Conservative 20; Mismatches 20; Indels 20; Gaps 5;
C;Keywords: alternative splicing; cytokine; glycoprotein

Qy 1 APPRLICDSRVLYRLLEAKENITTCAGHCSNENITVPDTKYNFYAKRMEVGGQA 60
Db 24 APP--ACDLRVLSKLLRDSHVLHSLSCQPEVHPPLTPVLLPAVDVSLGKNTQMEETKA 81
Qy 61 VEVWQGLALLSEAVL--RQALLVNSQWPWEPLQHFVDKAVSGLSRLTTLRALGAQKEA 118
Db 82 QDILGAVTLLLEGVWAARGQLGPTCLSSLLGQLSQVRLLLGALQSL-----LGTQ--- 132
Qy 119 ISPPDAASAAPLRTITADTFKRLFRVYSNFLRGK 154
Db 133 -LPPOG-----RTTAHKDPNAIFLSFQHLRGKVR 161

RESULT 12
80105
hombopoietin precursor - human
;Alternate names: c-MPL ligand; megakaryocyte growth and development factor precursor
;Species: Homo sapiens (man)
;Date: 24-May-1996 #sequence revision 24-May-1996 #text change 20-Jun-2000
;Accession: I59281; I80105; S45331; S48740; I38672; I52610
;Poster: D.C.; Sprecher, C.A.; Grant, F.J.; Kramer, J.M.; Kujper, J.L.; Holly, R.D.; W
roc. Natl. Acad. Sci. U.S.A. 91, 13023-13027, 1994
;Title: Human thrombopoietin: gene structure, cDNA sequence, expression, and chromosomal
;Reference number: I59281; MUID:95108091; PMID:7809166
;Accession: I59281
;Status: translated from GB/EMBL/DDBJ
;Molecule type: DNA
;Residues: 1-353 <RE2>
;Cross-references: GB:I36051; NID:G533214; PIDN:AAC37568.1; PID:G533215
;Accession: I80105
;Status: translated from GB/EMBL/DDBJ
;Molecule type: mRNA
;Residues: 1-353 <RE3>
;Cross-references: GB:I36052; NID:G533216; PIDN:AAC37566.1; PID:G533217
;Accession: S45331
;Status: preliminary
;Molecule type: mRNA
;Residues: 1-353 <SAU>
;Cross-references: GB:I33410; NID:G506826; PIDN:AAAS9857.1; PID:G506827
;Schma, Y.; Akahori, H.; Seki, N.; Hori, T.; Ogami, K.; Kato, T.; Shimada, Y.; Kawamura
EBS Lett. 353, 57-61, 1994
;Title: Molecular cloning and chromosomal localization of the human thrombopoietin gene
;Reference number: S48740; MUID:95010765; PMID:7926023
;Accession: S48740
;Status: preliminary
;Molecule type: DNA
;Residues: 1-353 <SOH>
;Cross-references: GB:D32046; NID:G577319; PIDN:BAAO6807.1; PID:G577320
;Bartley, T.D.; Bogenberger, J.; Hunt, P.; Li, Y.S.; Lu, H.S.; Martin, F.; Chang, M.S.;
elli 77, 1117-1124, 1994
;Title: Identification and cloning of a megakaryocyte growth and development factor tha
;Reference number: A54463; MUID:94291201; PMID:8020099
;Accession: I38672
;Status: preliminary
;Molecule type: mRNA
;Residues: 1-112, 'E', 114-353 <RE3>
;Cross-references: EMBL:U11025; NID:G511223; PIDN:AAAS0553.1; PID:G558078
;Gurney, A.L.; Huang, W.J.; Xie, M.H.; Malloy, B.E.; Eaton, D.L.; de Sauvage, F.J.
lood 85, 981-988, 1995
;Title: Genomic structure, chromosomal localization, and conserved alternative splice f
;Reference number: I52610; MUID:95152076; PMID:7849319
;Accession: I52610
;Status: preliminary; translated from GB/EMBL/DDBJ
;Molecule type: DNA
;Residues: 1-353 <RE4>
;Cross-references: GB:S76771; NID:G914225; PIDN:AAB33390.1; PID:G914226
;Genetics:
;Gene: GDB:THPO; MGDF
;Cross-references: GDB:374007; OMIM:600044

A;Map position: 3q26.3-3q27
A;Introns: 5/1; 47/3; 76/3; 132/3
C;Keywords: alternative splicing; cytokine; glycoprotein

Query Match 10.5%; Score 89; DB 2; Length 353;
Best Local Similarity 26.3%; Pred. No. 0.76; Mismatches 20; Indels 20; Gaps 5;
Matches 41; Conservative 20; Mismatches 20; Indels 20; Gaps 5;
C;Keywords: alternative splicing; cytokine; glycoprotein

Qy 1 APPRLICDSRVLYRLLEAKENITTCAGHCSNENITVPDTKYNFYAKRMEVGGQA 60
Db 24 APP--ACDLRVLSKLLRDSHVLHSLSCQPEVHPPLTPVLLPAVDVSLGKNTQMEETKA 81
Qy 61 VEVWQGLALLSEAVL--RQALLVNSQWPWEPLQHFVDKAVSGLSRLTTLRALGAQKEA 118
Db 82 QDILGAVTLLLEGVWAARGQLGPTCLSSLLGQLSQVRLLLGALQSL-----LGTQ--- 132
Qy 119 ISPPDAASAAPLRTITADTFKRLFRVYSNFLRGK 154
Db 133 -LPPOG-----RTTAHKDPNAIFLSFQHLRGKVR 161

RESULT 13
AB0323
ribonucleoside-diphosphate reductase (EC 1.17.4.1) beta chain [imported] - Yersinia pest:
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C;Accession: AB0323
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, I
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11596360
A;Accession: AB0323
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-323 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC92889.1; PID:G15980631; GSPDB:GN00175
C;Genetics:
A;Gene: nrdF
C;Superfamily: ribonucleoside-diphosphate reductase beta
C;Keywords: oxidoreductase

Query Match 10.4%; Score 88; DB 2; Length 323;
Best Local Similarity 25.2%; Pred. No. 0.85;
Matches 34; Conservative 20; Mismatches 59; Indels 22; Gaps 5;
C;Keywords: alternative splicing; cytokine; glycoprotein

Qy 38 NITVPDTKYNFYAKRMEVGGQAQAVSQGLALLSEAVLRGQALLVNSQWPWEPLQLHYD- 96
Db 2 NVVKPITRISAINNNKIE-DDKDLVNN--RUTSNFWLPKPVLSNDIPSWATLTPHEQQ 58
Qy 97 ---KAVSGLSRLTTLRALGAQ---KEAISPDAASAAPLRTITADTFKRLFRVYSNFLR 150
Db 59 LTRVFTGLTDTQNTLGAALIKDAITPHEAIFSNISFMBAVHARSYSIFSTL-- 116
Qy 151 GKULYTGACRTGD 165
Db 117 -----CLTSD 121

RESULT 14
AE0359
Solute binding receptor protein [imported] - Salmonella enterica subsp. enterica serovar
C;Species: Salmonella enterica subsp. enterica serovar typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AE0359
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Garra, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov:

Search completed: May 25, 2004, 11:23:33
Job time : 24 secs

GenCore version 5.1.6
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M protein - protein search, using sw model

run on: May 25, 2004, 11:23:05 ; Search time 43 Seconds
(without alignments)
1070.281 Million cell updates/sec

title: US-09-830-964-1
effect score: 846
sequence: 1 APRRLICDSRVLYLEAKE.....SNFLRGKLYTGACRTGD 165

coring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 1149313 seqs, 278921704 residues

total number of hits satisfying chosen parameters: 1149313

minimum DB seq length: 0
maximum DB seq length: 2000000000

post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- database : Published Applications AA.*
- 1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/prodata/2/pubpaa/BCT_NEW_PUB.pep.*
 - 3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/prodata/2/pubpaa/FCUS_PUBCOMB.pep.*
 - 7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep.*
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 - 10: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
 - 11: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
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 - 14: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	846	100.0	165	9	US-09-853-731-1
2	846	100.0	165	10	US-09-945-517-1
3	846	100.0	165	12	US-10-411-037-73
4	846	100.0	165	13	US-10-411-028-73
5	846	100.0	165	13	US-10-411-028-73
6	846	100.0	165	14	US-10-241-356-1
7	846	100.0	165	14	US-10-293-551-1
8	846	100.0	165	16	US-10-410-962-73
9	846	100.0	165	16	US-10-411-049-73
10	846	100.0	166	9	US-09-853-731-2
11	846	100.0	166	12	US-10-467-115-1
12	846	100.0	166	13	US-10-014-363-2
13	846	100.0	166	14	US-10-241-356-2
14	846	100.0	166	14	US-10-293-551-2
15	846	100.0	165	14	US-10-400-377-2

16	846	100.0	166	14	US-10-400-708-2	Sequence 2, Appli
17	846	100.0	166	14	US-10-298-148-2	Sequence 2, Appli
18	846	100.0	166	15	US-10-360-101-227	Sequence 227, App
19	846	100.0	169	13	US-10-014-363-4	Sequence 4, Appli
20	846	100.0	174	13	US-10-014-363-3	Sequence 3, Appli
21	846	100.0	174	13	US-10-014-363-5	Sequence 5, Appli
22	846	100.0	193	10	US-09-813-7750-4	Sequence 4, Appli
23	846	100.0	193	14	US-10-113-824-2	Sequence 2, Appli
24	846	100.0	209	14	US-10-230-454-4	Sequence 4, Appli
25	846	100.0	220	14	US-10-196-183-2	Sequence 2, Appli
26	846	100.0	370	14	US-10-230-454-3	Sequence 3, Appli
27	846	100.0	428	12	US-10-622-108-10	Sequence 10, Appli
28	846	100.0	428	15	US-10-435-608-10	Sequence 10, Appli
29	846	100.0	435	10	US-09-932-812-22	Sequence 22, Appli
30	846	100.0	436	10	US-08-932-812-18	Sequence 18, Appli
31	846	100.0	437	10	US-09-932-812-20	Sequence 20, Appli
32	843	99.6	193	12	US-10-622-108-4	Sequence 4, Appli
33	843	99.6	193	15	US-10-435-608-4	Sequence 4, Appli
34	843	99.6	412	10	US-09-775-964-34	Sequence 34, Appli
35	843	99.6	425	12	US-10-622-108-8	Sequence 8, Appli
36	843	99.6	425	15	US-10-435-608-8	Sequence 8, Appli
37	838	99.1	166	15	US-10-455-697-1	Sequence 1, Appli
38	838	99.1	166	16	US-10-291-847-214	Sequence 214, App
39	838	99.1	166	16	US-10-460-550-3	Sequence 3, Appli
40	838	99.1	193	10	US-09-813-7750-2	Sequence 2, Appli
41	838	99.1	193	12	US-10-411-037-16	Sequence 16, Appli
42	838	99.1	193	12	US-10-411-026-16	Sequence 16, Appli
43	838	99.1	193	12	US-10-609-346-16	Sequence 16, Appli
44	838	99.1	193	15	US-10-351-196-2	Sequence 2, Appli
45	838	99.1	193	15	US-10-463-980-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-853-731-1
; Sequence 1, Application US/09853731
; Patent No. US20020037841A1
; GENERAL INFORMATION:
; APPLICANT: Papadimitriou, Apollon
; TITLE OF INVENTION: Erythropoietin Composition
; FILE REFERENCE: 20619 US
; CURRENT APPLICATION NUMBER: US/09/853,731
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP/00110355.5
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Version 3.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-731-1

Query Match	100.0%	Score 846;	DB 9;	Length 165;
Best Local Similarity	100.0%	Fred. No. 5.7e-88;		
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Db	1	APRRLICDSRVLYLEAKEAENITTCGAECSCSNENITVPDITKVFYAKRMVEVGQQA	60	
QY	61	VEVWQGLALLSEAVLRGQALLVNSQPFEPYOLHYVDKAVSGLSRLTLRLALGAQKEAIS	120	
Db	61	VEVWQGLALLSEAVLRGQALLVNSQPFEPYOLHYVDKAVSGLSRLTLRLALGAQKEAIS	120	
QY	121	PPDAASAPLRTTTATDFKLFVYNSFLRGKLYTGACRTGD	165	
Db	121	PPDAASAPLRTTTATDFKLFVYNSFLRGKLYTGACRTGD	165	
RESULT 2				

JS-09-945-517-1
; Sequence 1, Application US/09945517
; Publication No. US20030104996A1
; GENERAL INFORMATION:
; APPLICANT: Chang, Byeong
; APPLICANT: Soley, Christopher
; TITLE OF INVENTION: L-METHIONINE AS A STABILIZER FOR NESP/EPO IN HSA-FREE FORMULATION
; FILE REFERENCE: A-803
; CURRENT APPLICATION NUMBER: US/09/945,517
; CURRENT FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
JS-09-945-517-1

Query Match 100.0%; Score 846; DB 10; Length 165;
Best Local Similarity 100.0%; Pred. No. 5.7e-88;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 APPRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKVNFKYAKRMEVGGQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVDAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVDAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAPLRTITADTFRKLFVYNSFLRGKLYTGEACRTGD 165
DB 121 PPDAASAPLRTITADTFRKLFVYNSFLRGKLYTGEACRTGD 165

RESULT 3
US-10-411-037-73
; Sequence 73, Application US/10411037
; Publication No. US2004004346A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
; FILE REFERENCE: 040853-01-5082
; CURRENT APPLICATION NUMBER: US/10/411,037
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-411-037-73

Query Match 100.0%; Score 846; DB 12; Length 165;
Best Local Similarity 100.0%; Pred. No. 5.7e-88;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKVNFKYAKRMEVGGQA 60
DB 1 APPRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKVNFKYAKRMEVGGQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVDAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVDAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAPLRTITADTFRKLFVYNSFLRGKLYTGEACRTGD 165
DB 121 PPDAASAPLRTITADTFRKLFVYNSFLRGKLYTGEACRTGD 165

RESULT 4

US-10-411-026-73
; Sequence 73, Application US/10411026
; Publication No. US20040063911A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; FILE REFERENCE: 040853-01-5053
; CURRENT APPLICATION NUMBER: US/10/411,026
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-026-73

Query Match 100.0%; Score 846; DB 12; Length 165;
Best Local Similarity 100.0%; Pred. No. 5.7e-88;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKVNFKYAKRMEVGGQA 60
DB 1 APPRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKVNFKYAKRMEVGGQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVDAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVDAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAPLRTITADTFRKLFVYNSFLRGKLYTGEACRTGD 165
DB 121 PPDAASAPLRTITADTFRKLFVYNSFLRGKLYTGEACRTGD 165

RESULT 5
 S-10-014-363-1
 ; Sequence 1, Application US/10014363
 ; Publication No. US20020115833A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Burg, Josef
 ; APPLICANT: Engel, Alfred
 ; APPLICANT: Franze, Reinhard
 ; APPLICANT: Hilger, Bernd
 ; APPLICANT: Schurig, Hartmut Ernst
 ; APPLICANT: Tischer, Wilhelm
 ; APPLICANT: Wozny, Manfred
 ; TITLE OF INVENTION: Erythropoietin Conjugates
 ; FILE REFERENCE: Case 20805
 ; CURRENT APPLICATION NUMBER: US/10/014,363
 ; CURRENT FILING DATE: 2001-12-11
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 165
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; S-10-014-363-1
 ; Query Match 100.0%; Score 846; DB 13; Length 165;
 ; Best Local Similarity 100.0%; Pred. No. 5.7e-88;
 ; Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ; Y 1 APPRLCDSRVLYRLLEAKEAENITTCAGHCSLNENITVPDTKVFYAKRMEVGQQA 60
 ; b 1 APPRLCDSRVLYRLLEAKEAENITTCAGHCSLNENITVPDTKVFYAKRMEVGQQA 60
 ; Y 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQVHVDKAVSGLSRLTLLRALGAQKEAIS 120
 ; b 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQVHVDKAVSGLSRLTLLRALGAQKEAIS 120
 ; Y 121 PPDAASAAPLRTITADTFKFLFRVYSNFIKGLKLYTGEACRTGD 165
 ; b 121 PPDAASAAPLRTITADTFKFLFRVYSNFIKGLKLYTGEACRTGD 165
 ; RESULT 6
 ; S-10-241-356-1
 ; Sequence 1, Application US/10241356
 ; Publication No. US2003007753A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TISCHER, WILHELM
 ; TITLE OF INVENTION: DIGLYCOSYLATED ERYTHROPOIETIN
 ; FILE REFERENCE: 20971
 ; CURRENT APPLICATION NUMBER: US/10/241,356
 ; CURRENT FILING DATE: 2002-09-11
 ; PRIOR APPLICATION NUMBER: EP 01122555.4
 ; PRIOR FILING DATE: 2001-09-25
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 165
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; S-10-241-356-1
 ; Query Match 100.0%; Score 846; DB 14; Length 165;
 ; Best Local Similarity 100.0%; Pred. No. 5.7e-88;
 ; Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ; Y 1 APPRLCDSRVLYRLLEAKEAENITTCAGHCSLNENITVPDTKVFYAKRMEVGQQA 60
 ; b 1 APPRLCDSRVLYRLLEAKEAENITTCAGHCSLNENITVPDTKVFYAKRMEVGQQA 60
 ; Y 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQVHVDKAVSGLSRLTLLRALGAQKEAIS 120
 ; b 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQVHVDKAVSGLSRLTLLRALGAQKEAIS 120
 ; Y 121 PPDAASAAPLRTITADTFKFLFRVYSNFIKGLKLYTGEACRTGD 165
 ; b 121 PPDAASAAPLRTITADTFKFLFRVYSNFIKGLKLYTGEACRTGD 165
 ; RESULT 7
 ; US-10-293-551-1
 ; Sequence 1, Application US/10293551
 ; Publication No. US20030120045A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bailon, Pascal
 ; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
 ; FILE REFERENCE: 1097 nonprovisional
 ; CURRENT APPLICATION NUMBER: US/10/293,551
 ; CURRENT FILING DATE: 2002-11-14
 ; PRIOR APPLICATION NUMBER: US/09/604,938
 ; PRIOR FILING DATE: 2000-08-27
 ; PRIOR APPLICATION NUMBER: 60/166,151
 ; PRIOR FILING DATE: 1999-11-17
 ; PRIOR APPLICATION NUMBER: 60/151,548
 ; PRIOR FILING DATE: 1999-08-13
 ; PRIOR APPLICATION NUMBER: 60/150,225
 ; PRIOR FILING DATE: 1999-08-23
 ; PRIOR APPLICATION NUMBER: 60/142,254
 ; PRIOR FILING DATE: 1999-07-02
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 165
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-293-551-1
 ; Query Match 100.0%; Score 846; DB 14; Length 165;
 ; Best Local Similarity 100.0%; Pred. No. 5.7e-88;
 ; Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ; Y 1 APPRLCDSRVLYRLLEAKEAENITTCAGHCSLNENITVPDTKVFYAKRMEVGQQA 60
 ; b 1 APPRLCDSRVLYRLLEAKEAENITTCAGHCSLNENITVPDTKVFYAKRMEVGQQA 60
 ; Y 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQVHVDKAVSGLSRLTLLRALGAQKEAIS 120
 ; b 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQVHVDKAVSGLSRLTLLRALGAQKEAIS 120
 ; Y 121 PPDAASAAPLRTITADTFKFLFRVYSNFIKGLKLYTGEACRTGD 165
 ; b 121 PPDAASAAPLRTITADTFKFLFRVYSNFIKGLKLYTGEACRTGD 165
 ; RESULT 8
 ; US-10-410-962-73
 ; Sequence 73, Application US/10410962
 ; Publication No. US20040077836A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Neose Technologies, Inc.
 ; APPLICANT: DePree, Shawn
 ; APPLICANT: Zopf, David
 ; APPLICANT: Bayer, Robert
 ; APPLICANT: Hakes, David
 ; APPLICANT: Chen, Xi
 ; APPLICANT: Bowe, Caryn
 ; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
 ; TITLE OF INVENTION: GLYCOCONJUGATION OF G-CSF
 ; FILE REFERENCE: 040853-01-5054
 ; CURRENT APPLICATION NUMBER: US/10/410,962
 ; CURRENT FILING DATE: 2003-04-09
 ; PRIOR APPLICATION NUMBER: US 60/328,523
 ; PRIOR FILING DATE: 2001-10-10
 ; PRIOR APPLICATION NUMBER: US 60/344,692
 ; PRIOR FILING DATE: 2001-10-19
 ; PRIOR APPLICATION NUMBER: US 60/387,292

RESULT 5
 S-10-014-363-1
 ; Sequence 1, Application US/10014363
 ; Publication No. US20020115833A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Burg, Josef
 ; APPLICANT: Engel, Alfred
 ; APPLICANT: Franze, Reinhard
 ; APPLICANT: Hilger, Bernd
 ; APPLICANT: Schurig, Hartmut Ernst
 ; APPLICANT: Tischer, Wilhelm
 ; APPLICANT: Wozny, Manfred
 ; TITLE OF INVENTION: Erythropoietin Conjugates
 ; FILE REFERENCE: Case 20805
 ; CURRENT APPLICATION NUMBER: US/10/014,363
 ; CURRENT FILING DATE: 2001-12-11
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 165
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; S-10-014-363-1
 ; Query Match 100.0%; Score 846; DB 13; Length 165;
 ; Best Local Similarity 100.0%; Pred. No. 5.7e-88;
 ; Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ; Y 1 APPRLCDSRVLYRLLEAKEAENITTCAGHCSLNENITVPDTKVFYAKRMEVGQQA 60
 ; b 1 APPRLCDSRVLYRLLEAKEAENITTCAGHCSLNENITVPDTKVFYAKRMEVGQQA 60
 ; Y 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQVHVDKAVSGLSRLTLLRALGAQKEAIS 120
 ; b 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQVHVDKAVSGLSRLTLLRALGAQKEAIS 120
 ; Y 121 PPDAASAAPLRTITADTFKFLFRVYSNFIKGLKLYTGEACRTGD 165
 ; b 121 PPDAASAAPLRTITADTFKFLFRVYSNFIKGLKLYTGEACRTGD 165
 ; RESULT 6
 ; S-10-241-356-1
 ; Sequence 1, Application US/10241356
 ; Publication No. US2003007753A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TISCHER, WILHELM
 ; TITLE OF INVENTION: DIGLYCOSYLATED ERYTHROPOIETIN
 ; FILE REFERENCE: 20971
 ; CURRENT APPLICATION NUMBER: US/10/241,356
 ; CURRENT FILING DATE: 2002-09-11
 ; PRIOR APPLICATION NUMBER: EP 01122555.4
 ; PRIOR FILING DATE: 2001-09-25
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 165
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; S-10-241-356-1
 ; Query Match 100.0%; Score 846; DB 14; Length 165;
 ; Best Local Similarity 100.0%; Pred. No. 5.7e-88;
 ; Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ; Y 1 APPRLCDSRVLYRLLEAKEAENITTCAGHCSLNENITVPDTKVFYAKRMEVGQQA 60
 ; b 1 APPRLCDSRVLYRLLEAKEAENITTCAGHCSLNENITVPDTKVFYAKRMEVGQQA 60
 ; Y 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQVHVDKAVSGLSRLTLLRALGAQKEAIS 120
 ; b 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQVHVDKAVSGLSRLTLLRALGAQKEAIS 120

Query Match 100.0%; Score 846; DB 16; Length 165;
Best Local Similarity 100.0%; Pred. No. 5.7e-88;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLCDSEVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVGGQA 60
DB 1 APPRLCDSEVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVGGQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGKLYTGEACRTGD 165
DB 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGKLYTGEACRTGD 165
RESULT 10
US-09-853-731-2
; Sequence 2, Application US/09853731
; Patent No. US20020037841A1
; GENERAL INFORMATION:
; APPLICANT: Papadimitriou, Apollon
; TITLE OF INVENTION: Erythropoietin Composition
; FILE REFERENCE: 20619 US
; CURRENT APPLICATION NUMBER: US/09/853,731
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP/00110355.5
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-731-2
Query Match 100.0%; Score 846; DB 9; Length 166;
Best Local Similarity 100.0%; Pred. No. 5.7e-88;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLCDSEVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVGGQA 60
DB 1 APPRLCDSEVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVGGQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGKLYTGEACRTGD 165
DB 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGKLYTGEACRTGD 165
RESULT 11
US-10-467-115-1
; Sequence 1, Application US/10467115
; Publication No. US20040063917A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; TITLE OF INVENTION: MODIFIED ERYTHROPOIETIN (EPO) WITH
; FILE REFERENCE: MER-114
; CURRENT APPLICATION NUMBER: US/10/467,115
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: 01102615.0
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: PCT/EP02/01174

PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 73
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-962-73
Query Match 100.0%; Score 846; DB 16; Length 165;
Best Local Similarity 100.0%; Pred. No. 5.7e-88;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLCDSEVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVGGQA 60
DB 1 APPRLCDSEVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVGGQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGKLYTGEACRTGD 165
DB 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGKLYTGEACRTGD 165
RESULT 9
US-10-411-049-73
; Sequence 73, Application US/10411049
; Publication No. US20040082026A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Howe, Caryn
; TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; FILE REFERENCE: 040853-01-5055
; CURRENT APPLICATION NUMBER: US/10/411,049
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 73
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-049-73

PRIOR FILING DATE: 2002-02-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
S-10-467-115-1

Query Match 100.0%; Score 846; DB 12; Length 166;
Best Local Similarity 100.0%; Pred. No. 5.7e-88;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 APRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 60
b 1 APRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 60
Y 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
b 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
Y 121 PPDAASAPLRITITADTFRKLFVYSNFRGKLYTGACRTGD 165
b 121 PPDAASAPLRITITADTFRKLFVYSNFRGKLYTGACRTGD 165

RESULT 12
S-10-014-363-2
Sequence 2, Application US/10014363
Publication No. US20020115833A1
GENERAL INFORMATION:
APPLICANT: Burg, Josef
APPLICANT: Engel, Alfred
APPLICANT: Franze, Reinhard
APPLICANT: Hilger, Bernd
APPLICANT: Schurig, Hartmut Ernst
APPLICANT: Tischer, Wilhelm
APPLICANT: Wozny, Manfred
TITLE OF INVENTION: Erythropoietin Conjugates
FILE REFERENCE: Case 20805
CURRENT APPLICATION NUMBER: US/10/014,363
CURRENT FILING DATE: 2001-12-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
S-10-014-363-2

Query Match 100.0%; Score 846; DB 13; Length 166;
Best Local Similarity 100.0%; Pred. No. 5.7e-88;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 APRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 60
b 1 APRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 60
Y 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
b 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
Y 121 PPDAASAPLRITITADTFRKLFVYSNFRGKLYTGACRTGD 165
b 121 PPDAASAPLRITITADTFRKLFVYSNFRGKLYTGACRTGD 165

RESULT 13
S-10-241-356-2
Sequence 2, Application US/10241356
Publication No. US2003007753A1
GENERAL INFORMATION:
APPLICANT: TISCHER, WILHELM

TITLE OF INVENTION: DIGLYCOSYLATED ERYTHROPOIETIN
FILE REFERENCE: 20971
CURRENT APPLICATION NUMBER: US/10/241,356
CURRENT FILING DATE: 2002-09-11
PRIOR APPLICATION NUMBER: EP 01122555.4
PRIOR FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
US-10-241-356-2

Query Match 100.0%; Score 846; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 5.7e-88;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 60
Db 1 APRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAPLRITITADTFRKLFVYSNFRGKLYTGACRTGD 165
Db 121 PPDAASAPLRITITADTFRKLFVYSNFRGKLYTGACRTGD 165

RESULT 14
US-10-293-551-2
Sequence 2, Application US/10293551
Publication No. US20030120045A1
GENERAL INFORMATION:
APPLICANT: Ballon, Pascal
TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
FILE REFERENCE: 1097 nonprovisional
CURRENT APPLICATION NUMBER: US/10/293,551
CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: US/09/604,938
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/166,151
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/151,548
PRIOR FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: 60/150,225
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: 60/142,254
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-551-2

Query Match 100.0%; Score 846; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 5.7e-88;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 60
Db 1 APRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAPLRITITADTFRKLFVYSNFRGKLYTGACRTGD 165

Db 121 PPDAASAPLRTITADTRKLFVYSNPLRGKLYTGEACRTGD 165

RESULT 15

US-10-400-377-2

; Sequence, Application US/10400377

; Publication No. US20030162949A1

; GENERAL INFORMATION:

; APPLICANT: Cox III, George N

; APPLICANT: Bolder Biotechnology, Inc.

; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins

; FILE REFERENCE: 4152-1-PUS

; CURRENT APPLICATION NUMBER: US/10/400,377

; CURRENT FILING DATE: 2003-03-26

; PRIOR APPLICATION NUMBER: US/09/462,941

; PRIOR FILING DATE: 2000-01-14

; PRIOR APPLICATION NUMBER: 60/052,516

; PRIOR FILING DATE: 1997-07-14

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 166

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-400-377-2

Query Match 100.0%; Score 846; DB 14; Length 166;

Best Local Similarity 100.0%; Pred. No. 5.7e-88;

Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLEAKEAENITTCGAEHCNENITVPDTKVNIFYAKRMEVGGQA 60

Db 1 APPRLICDSRVLYRLLEAKEAENITTCGAEHCNENITVPDTKVNIFYAKRMEVGGQA 60

QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSITTLRALGAQKEAIS 120

Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSITTLRALGAQKEAIS 120

QY 121 PPDAASAPLRTITADTRKLFVYSNPLRGKLYTGEACRTGD 165

Db 121 PPDAASAPLRTITADTRKLFVYSNPLRGKLYTGEACRTGD 165

Search completed: May 25, 2004, 11:28:52

Job time : 44 secs

M protein - protein search, using sw model

run on: May 25, 2004, 11:20:29 ; Search time 23 Seconds
(without alignments)
370.360 Million cell updates/sec

title: US-09-830-964-1
subject score: 846
sequence: 1 APPRLICDSRVLYRLLLEAK.....SNFLRGKLYTGACRTGD 165

scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 389414 seqs, 51625971 residues

total number of hits satisfying chosen parameters: 389414

minimum DB seq length: 0
maximum DB seq length: 2000000000

post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

database : Issued_Patents_AA:*
1: /cgn2_6/prodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/iaa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	% Match	Query Length	ID	Description
1	846	100.0	165	4	US-09-604-871-1 Sequence 1, Appli
2	846	100.0	165	4	US-09-604-938-1 Sequence 1, Appli
3	846	100.0	166	1	US-08-318-193-70 Sequence 70, Appli
4	846	100.0	166	4	US-09-604-871-2 Sequence 2, Appli
5	846	100.0	166	4	US-09-604-938-2 Sequence 2, Appli
6	846	100.0	166	4	US-09-462-941-2 Sequence 2, Appli
7	846	100.0	166	5	PCT-US94-04361-37 Sequence 37, Appli
8	846	100.0	193	1	US-07-903-220-1 Sequence 1, Appli
9	846	100.0	193	2	US-08-883-795A-34 Sequence 34, Appli
10	846	100.0	193	4	US-09-552-265B-4 Sequence 4, Appli
11	843	99.6	165	4	US-09-554-451-8 Sequence 8, Appli
12	843	99.6	412	4	US-09-366-009-34 Sequence 34, Appli
13	843	99.6	412	4	US-08-809-156B-34 Sequence 34, Appli
14	838	99.1	193	4	US-09-552-265B-2 Sequence 2, Appli
15	834	98.6	193	4	US-09-552-265B-5 Sequence 5, Appli
16	830	98.1	166	5	PCT-US94-04361-45 Sequence 45, Appli
17	825	97.5	166	4	US-09-552-265B-30 Sequence 30, Appli
18	825	97.5	193	4	US-09-552-265B-46 Sequence 46, Appli
19	824	97.4	166	4	US-09-552-265B-22 Sequence 22, Appli
20	824	97.4	166	4	US-09-552-265B-38 Sequence 38, Appli
21	824	97.4	193	4	US-09-552-265B-38 Sequence 38, Appli
22	824	97.4	193	4	US-09-552-265B-48 Sequence 48, Appli
23	822	97.2	166	4	US-09-552-265B-20 Sequence 20, Appli
24	822	97.2	166	4	US-09-552-265B-24 Sequence 24, Appli
25	822	97.2	193	4	US-09-552-265B-36 Sequence 36, Appli
26	822	97.2	193	4	US-09-552-265B-40 Sequence 40, Appli
27	821	97.0	166	4	US-09-552-265B-26 Sequence 26, Appli

28	821	97.0	166	4	US-09-552-265B-31 Sequence 31, Appli
29	821	97.0	193	4	US-09-552-265B-42 Sequence 42, Appli
30	821	97.0	193	4	US-09-552-265B-47 Sequence 47, Appli
31	820	96.9	166	4	US-09-552-265B-18 Sequence 18, Appli
32	820	96.9	166	4	US-09-552-265B-23 Sequence 23, Appli
33	820	96.9	166	4	US-09-552-265B-28 Sequence 28, Appli
34	820	96.9	166	4	US-09-552-265B-33 Sequence 33, Appli
35	820	96.9	193	4	US-09-552-265B-34 Sequence 34, Appli
36	820	96.9	193	4	US-09-552-265B-39 Sequence 39, Appli
37	820	96.9	193	4	US-09-552-265B-44 Sequence 44, Appli
38	820	96.9	193	4	US-09-552-265B-49 Sequence 49, Appli
39	818	96.7	166	4	US-09-552-265B-21 Sequence 21, Appli
40	818	96.7	166	4	US-09-552-265B-25 Sequence 25, Appli
41	818	96.7	193	4	US-09-552-265B-37 Sequence 37, Appli
42	818	96.7	193	4	US-09-552-265B-41 Sequence 41, Appli
43	817	96.6	166	4	US-09-552-265B-27 Sequence 27, Appli
44	817	96.6	193	4	US-09-552-265B-43 Sequence 43, Appli
45	816	96.5	166	4	US-09-552-265B-19 Sequence 19, Appli

ALIGNMENTS

RESULT 1
US-09-604-871-1

; Sequence 1, Application US/09604871
; Patent No. 6340742

; GENERAL INFORMATION:

; APPLICANT: Bug, Josef

; APPLICANT: Hilger, Bernd

; APPLICANT: Josel, Hans-Peter

; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES

; FILE REFERENCE: 1098 nonprovisional

; CURRENT APPLICATION NUMBER: US/09/604,871

; CURRENT FILING DATE: 2000-06-28

; PRIOR APPLICATION NUMBER: 60/151,454

; PRIOR FILING DATE: 1999-08-30

; PRIOR APPLICATION NUMBER: 60/147,452

; PRIOR FILING DATE: 1999-08-05

; PRIOR APPLICATION NUMBER: 60/142,243

; PRIOR FILING DATE: 1999-07-02

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 1

; LENGTH: 165

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-604-871-1

Query Match 100.0%; Score 846; DB 4; Length 165;

Best Local Similarity 100.0%; Pred. No. 1.1e-99; Mismatches 0; Indels 0; Gaps 0;

Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKAENITTCABHCSLNENITVPDTKWNFYAKRMEVGQQA 60

DB 1 APPRLICDSRVLYRLLLEAKAENITTCABHCSLNENITVPDTKWNFYAKRMEVGQQA 60

QY 61 VEVWQGLALLSEAVLRGQALLVNSSQWPEIQLHVDKAVSGIRSLTLLRALGAKQKAIS 120

DB 61 VEVWQGLALLSEAVLRGQALLVNSSQWPEIQLHVDKAVSGIRSLTLLRALGAKQKAIS 120

QY 121 PPDAAASAPLRITATDTFKLFRVYSNFRGLKLYTGACRTGD 165

DB 121 PPDAAASAPLRITATDTFKLFRVYSNFRGLKLYTGACRTGD 165

RESULT 2

US-09-604-938-1

; Sequence 1, Application US/09604938

; Patent No. 6583272

; GENERAL INFORMATION:

; APPLICANT: Bailion, Pascal

; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES

FILE REFERENCE: 1097 nonprovisional
CURRENT APPLICATION NUMBER: US/09/604,938
CURRENT FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/166,151
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/151,548
PRIOR FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: 60/150,225
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: 60/142,254
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 165
TYPE: PRT
ORGANISM: Homo sapiens
US-09-604-938-1

Query Match 100.0%; Score 846; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.1e-99;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNFYAKRMEVGQQA 60
DB 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNFYAKRMEVGQQA 60

QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120

QY 121 PPDAASAAPLRTITADTFRKLFVYSNFRGKLYTGEACRTGD 165
DB 121 PPDAASAAPLRTITADTFRKLFVYSNFRGKLYTGEACRTGD 165

RESULT 3
US-08-318-193-70
Sequence 70, Application US/08318193
Patent No. 5641663
GENERAL INFORMATION:
APPLICANT: GARVIN, Robert T.
APPLICANT: MALEK, Lawrence T.
TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION
TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY
TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,193
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,314
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 18740/116 CACO
TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-318-193-70

Query Match 100.0%; Score 846; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.1e-99;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNFYAKRMEVGQQA 60
DB 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNFYAKRMEVGQQA 60

QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120

QY 121 PPDAASAAPLRTITADTFRKLFVYSNFRGKLYTGEACRTGD 165
DB 121 PPDAASAAPLRTITADTFRKLFVYSNFRGKLYTGEACRTGD 165

RESULT 4
US-09-604-871-2
Sequence 2, Application US/09604871
Patent No. 6340742
GENERAL INFORMATION:
APPLICANT: Bug, Josef
APPLICANT: Hilger, Bernd
APPLICANT: Josel, Hans-Peter
TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
FILE REFERENCE: 1098 nonprovisional
CURRENT APPLICATION NUMBER: US/09/604,871
CURRENT FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/151,454
PRIOR FILING DATE: 1999-08-30
PRIOR APPLICATION NUMBER: 60/147,452
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 60/142,243
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
US-09-604-871-2

Query Match 100.0%; Score 846; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.1e-99;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNFYAKRMEVGQQA 60
DB 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNFYAKRMEVGQQA 60

QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120

QY 121 PPDAASAAPLRTITADTFRKLFVYSNFRGKLYTGEACRTGD 165
DB 121 PPDAASAAPLRTITADTFRKLFVYSNFRGKLYTGEACRTGD 165

RESULT 5
US-09-604-938-2

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

M protein - protein search, using sw model

run on: May 25, 2004, 11:15:13 ; Search time 58 Seconds
(without alignments)
803.799 Million cell updates/sec

title: US-09-830-964-1

affect score: 846

sequence: 1 APPRLCDSRVLEK...SNFLRGLKLTGACRTGD 165

scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

sarched: 1586107 seqs, 282547505 residues

otal number of hits satisfying chosen parameters: 1586107

imum DB seq length: 0

imum DB seq length: 200000000

et-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase :

A_Geneseq_29Jan04.*

1: Geneseqp19808.*

2: Geneseqp19908.*

3: Geneseqp20008.*

4: Geneseqp20018.*

5: Geneseqp20028.*

6: Geneseqp20038.*

7: Geneseqp20038s.*

8: Geneseqp20048.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	846	100.0	165	3	AAY93445 Amino aci
2	846	100.0	165	3	AAB03760 Human ery
3	846	100.0	165	3	AAY94605 Human ery
4	846	100.0	165	3	AAY99705 Non-glyco
5	846	100.0	165	4	AAB84525 Amino aci
6	846	100.0	165	4	ABB83621 Protein #
7	846	100.0	165	4	AAB66697 Human ery
8	846	100.0	165	5	AAM53061 Human ery
9	846	100.0	165	5	ABB77896 Amino aci
10	846	100.0	165	6	ABP98492 Amino aci
11	846	100.0	165	6	ABR39995 Human ery
12	846	100.0	166	1	AAP70398 Sequence
13	846	100.0	166	1	AAR23593 Recombina
14	846	100.0	166	2	AAM58404 Human ery
15	846	100.0	166	2	AAM77780 Human EPO
16	846	100.0	166	3	ABO7030 Modified
17	846	100.0	166	4	ABB83622 Protein #
18	846	100.0	166	4	AAB02641 Human ery
19	846	100.0	166	4	AAB66698 Human ery
20	846	100.0	166	5	ABG92101 Human ery
21	846	100.0	166	5	AAM53062 Human ery
22	846	100.0	166	5	ABB77897 Amino aci
23	846	100.0	166	6	ABR39996 Human ery
24	846	100.0	166	6	ABR57500 Human ery
25	846	100.0	167	1	AAP50299 Human rec

26	846	100.0	167	1	AAP50298 Human rec
27	846	100.0	169	5	ABB77899 Amino aci
28	846	100.0	174	5	ABB77898 Amino aci
29	846	100.0	174	5	ABB77900 Amino aci
30	846	100.0	188	1	AAP60599 Clone lam
31	846	100.0	188	1	AAP81195 Erythropro
32	846	100.0	193	1	AAP50300 Human ery
33	846	100.0	193	1	AAP60597 Clone lam
34	846	100.0	193	1	AAP70256 Sequence
35	846	100.0	193	2	AAR65499 Human pre
36	846	100.0	193	2	AAR71137 Human ery
37	846	100.0	193	2	AAR74141 Human ery
38	846	100.0	193	2	AAR81982 Human ery
39	846	100.0	193	2	AAR98397 Human ery
40	846	100.0	193	3	AAY43398 Human ery
41	846	100.0	193	3	AAY94530 Human ery
42	846	100.0	193	3	AAY93638 Amino aci
43	846	100.0	193	3	AAY99704 Human non
44	846	100.0	193	4	AAB34978 Human ery
45	846	100.0	193	4	AAB85573 Human ery

ALIGNMENTS

RESULT 1
AAY93445
ID AAY93445 standard; protein; 165 AA.
XX
AC AAY93445;
XX
DT 04-SEP-2000 (first entry)
XX
DE Amino acid sequence of human erythropoietin.
XX
KW Human; erythropoietin; EPO; anaemia; renal failure.
XX
OS Homo sapiens.
XX
PN WO200028066-A1.
PD
PP 18-MAY-2000.
XX
PF 08-NOV-1999; 99WO-US026238.
XX
PR 06-NOV-1998; 98AR-00105609.
PR 23-FEB-1999; 99AR-00100679.
XX
(STER-) STERRENHELD BIOTECHNOLOGIE NORTH AMERICA.
XX
PA Carcagno CM, Criscuolo M, Melo C, Vidal JA;
XX
PI WPI; 2000-376574/32.
XX
DR New host cell producing recombinant human erythropoietin (EPO) used for large scale production of EPO.
PT
XX
PS Claim 1; Page 26-27; 51pp; English.
XX
CC The present sequence represents human erythropoietin protein. The specification describes a host cell line which is used to produce human erythropoietin (EPO). EPO is a glycoprotein. The cell line is used for the production of recombinant human erythropoietin. The protein is used for the treatment of anaemia, especially anaemia derived from renal failure

SQ Sequence 165 AA;

Query Match 100.0%; Score 846; DB 3; Length 165;

Best Local Similarity 100.0%; Pred. No. 1.3e-86;

Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPRLCDSRVLEKAEENITTCACRCHSLNENITVPTTKVNFYAKRMEVGGQA 60

Db 1 APPRLCDSRVLYRLLLEAKEAENITTCAGHCSLNENITVPDTKVFYAKRMEVGQQA 60
61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHLVDKAVSGLSLTLRALGQKEAIS 120
61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHLVDKAVSGLSLTLRALGQKEAIS 120
121 PPDAASAAPLRTITADTFRKLFRVYSNFRGKLYTGACRTGD 165
121 PPDAASAAPLRTITADTFRKLFRVYSNFRGKLYTGACRTGD 165

RESULT 2
AAB03760
ID AAB03760 standard; protein; 165 AA.
AC AAB03760;
XX 04-OCT-2000 (first entry)
XX Human erythropoietin (EPO) amino acid sequence.
XX Erythropoietin; EPO; human; erythroblast differentiation; anaemia;
XX large scale production; renal failure.
XX Homo sapiens.
XX WO200027997-A1.
XX 18-MAY-2000.
XX 08-NOV-1999; 95WO-US026240.
XX 06-NOV-1998; 98AR-00105611.
XX 23-FEB-1999; 99AR-00100681.
XX (STER-) STERRENBELD BIOTECHNOLOGIE NORTH AMERICA.
XX Carcagno CM, Criscuolo M, Melo C, Vidal JA;
XX WPI; 2000-376519/32.
XX A novel method for the massive culture of recombinant mammalian cells
XX producing recombinant human erythropoietin.
XX Example 8; Page 11-12; 23pp; English.
XX This sequence represents the human erythropoietin amino acid sequence.
XX Erythropoietin is a glycoprotein that stimulates erythroblast
XX differentiation in the bone marrow. The present invention relates to a
XX method for the large scale production of human EPO from recombinant
XX mammalian cells. The method comprises culturing mammalian cells which
XX express recombinant human EPO in culture medium comprising insulin.
XX Erythropoietin can be used to treat anaemia derived from renal failure.
XX The method allows for the industrial scale production of EPO, and
XX overcomes the problems of low reproducibility and output quality which
XX are encountered with previous production methods
XX Sequence 165 AA;
SQ
Query Match 100.0%; Score 846; DB 3; Length 165;
Best Local Similarity 100.0%; Pred. NO. 1.3e-86; Indels 0; Gaps 0;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLCDSRVLYRLLLEAKEAENITTCAGHCSLNENITVPDTKVFYAKRMEVGQQA 60
DB 1 APPRLCDSRVLYRLLLEAKEAENITTCAGHCSLNENITVPDTKVFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHLVDKAVSGLSLTLRALGQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHLVDKAVSGLSLTLRALGQKEAIS 120
QY 121 PPDAASAAPLRTITADTFRKLFRVYSNFRGKLYTGACRTGD 165

Db 121 PPDAASAAPLRTITADTFRKLFRVYSNFRGKLYTGACRTGD 165
RESULT 3
AAY94605
ID AAY94605 standard; protein; 165 AA.
AC AAY94605;
XX 28-NOV-2000 (first entry)
XX Human erythropoietin.
XX Human; erythropoietin; EPO; purification; anaemia.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Modified-site 24 /note= "N-Glycosylation site"
XX Modified-site 38 /note= "N-Glycosylation site"
XX Modified-site 83 /note= "N-Glycosylation site"
XX Modified-site 126 /note= "N-Glycosylation site"
XX Modified-site /note= "O-Glycosylation site"
XX WO200027869-A1.
XX 18-MAY-2000.
XX 08-NOV-1999; 99WO-US026241.
XX 06-NOV-1998; 98AR-00105610.
XX 23-FEB-1999; 99AR-00100680.
XX (STER-) STERRENBELD BIOTECHNOLOGIE NORTH AMERICA.
XX Carcagno CM, Criscuolo M, Melo C, Vidal JA;
XX WPI; 2000-376485/32.
XX Novel methods for purifying recombinant human erythropoietin from
XX mammalian cell culture reagents.
XX Claim 16; Page 18; 30pp; English.
XX The present invention relates to a method for purifying erythropoietin
XX (EPO) for treatment of disease, especially anaemia. The method involves
XX treating cell culture supernatants with differential precipitation,
XX hydrophobic interaction chromatography, diafiltration, anionic and
XX cationic exchange chromatography and molecular exclusion chromatography.
XX The present sequence is the protein from the culture supernatant of
XX transfected cell lines after purification by the above process. The
XX sequence shows total homology with natural human EPO. The advantage of
XX this method is that high purity and quality EPO is produced. A further
XX advantage is that the process does not involve the use of organic
XX solvents that may harm the environment
XX Sequence 165 AA;
SQ
Query Match 100.0%; Score 846; DB 3; Length 165;
Best Local Similarity 100.0%; Pred. NO. 1.3e-86; Indels 0; Gaps 0;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLCDSRVLYRLLLEAKEAENITTCAGHCSLNENITVPDTKVFYAKRMEVGQQA 60
DB 1 APPRLCDSRVLYRLLLEAKEAENITTCAGHCSLNENITVPDTKVFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHLVDKAVSGLSLTLRALGQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHLVDKAVSGLSLTLRALGQKEAIS 120

QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAKQEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAKQEAIS 120
QY 121 PPDAASAAPLRTITADTPFKLFRVYSNFRGKGLKLYTGEACRTGD 165
Db 121 PPDAASAAPLRTITADTPFKLFRVYSNFRGKGLKLYTGEACRTGD 165

RESULT 5

AAB84525
ID AAB84525 standard; protein; 165 AA.

XX AC AAB84525;
XX DT 05-SEP-2001 (first entry)

XX DE Amino acid sequence of human erythropoietin (EPO) protein.
XX KW Erythropoietin; EPO; erythropoietin stimulating protein; NESP;
XX OS Sustained release.

XX PN Homo sapiens.

XX PD WO200130320-A1.

XX PF 03-MAY-2001.

XX PR 23-OCT-2000; 2000WO-US029257.

XX PR 22-OCT-1999; 99US-00426566.

XX PR 13-OCT-2000; 2000US-00687981.

XX PA (AMGE-) AMGEN INC.

XX PI Burke P, Klumb L, Murphy K, Herberger J, French DL;

XX DR WPI; 2001-417552/44.

XX PT Sustained release composition comprises an active biological ingredient,
XX PT notably a protein or other biopolymer, particularly erythropoietin
XX PT stimulating protein, in biocompatible, biodegradable polymeric
XX PT microparticles.

XX PS Disclosure; Page 56; 61pp; English.

XX CC The present sequence encodes a human erythropoietin (EPO) protein. The
XX CC specification describes a composition for the sustained release of
XX CC biologically active EPO stimulating protein (NESP). The reduced frequency
XX CC of administration of NESP, which requires preferably injection by skilled
XX CC personnel, improves patient compliance. Also, sustained release reduces
XX CC the nature and severity of any side effects of the drug

XX SQ Sequence 165 AA;

Query Match 100.0%; Score 846; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.3e-86;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKEENITTCGAHCSLNENITVPDKVNFYAWKRMVEVGQA 60
Db 1 APPRLICDSRVLYRLLLEAKEENITTCGAHCSLNENITVPDKVNFYAWKRMVEVGQA 60

QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAKQEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAKQEAIS 120

QY 121 PPDAASAAPLRTITADTPFKLFRVYSNFRGKGLKLYTGEACRTGD 165

Db 121 PPDAASAAPLRTITADTPFKLFRVYSNFRGKGLKLYTGEACRTGD 165

RESULT 6

Y 121 PPDAASAAPLRTITADTPFKLFRVYSNFRGKGLKLYTGEACRTGD 165
b 121 PPDAASAAPLRTITADTPFKLFRVYSNFRGKGLKLYTGEACRTGD 165

RESULT 4

AAY99705
D AAY99705 standard; protein; 165 AA.

C AAY99705;

T 15-SEP-2000 (first entry)

E Non-glycosylated erythropoietin analogue NGE-166delta.

X Human; non-glycosylated erythropoietin analogue; NGEA; haematocrit;
W antianaemic; anaemia; erythropoiesis promoter; mutant; mutin.

X Homo sapiens.

S Synthetic.

X WO200032772-A2.

N 08-JUN-2000.

D 23-NOV-1999; 99WO-US027801.

F 30-NOV-1998; 98US-0110289P.

R (ELIL) LILLY & CO ELI.

A Beals JM, Glaesner W, Micanovic R, Millican RL, Witcher DR;

I WPI; 2000-412320/35.

X N-PSDB; AAA48373.

X Non-glycosylated erythropoietic compound useful for increasing hematocrit
T level in mammal with insufficient hematocrit levels in conditions such as
T anemia, comprises protein covalently bonded to polymer.

X Claim 2; Page 93-94; 94pp; English.

X The present sequence is a non-glycosylated erythropoietin analogue (NGEA)
C designated NGE-166delta. The protein sequence is identical to the
C sequence of wild-type human non-glycosylated erythropoietin NGE except
C that Arg at position 166 is deleted. NGE promotes erythropoiesis and can
C therefore be used to increase haematocrit levels in mammals with
C conditions such as anaemia, in which levels of haematocrit are
C insufficient. NGE analogues can also be used to treat such conditions.
C NGEAs do not themselves cause a significant increase in haematocrit but
C they acquire that property once they are derivatised with polyethylene
C glycol polymers. The analogues can be produced using a linkerless
C aldehyde modification process. They show stability and bioactivity in
C vivo. The nucleotide sequence encoding this protein was constructed
C synthetically by in vitro hybridisation using a set of six overlapping
C oligonucleotides from the positive strand of human erythropoietin cDNA
C with six complementary oligonucleotides (negative strand). The codon
C usage was 100% optimised for E. coli codon usage. The hybridised
C oligonucleotides were ligated with T4 DNA ligase and the ligation product
C amplified by PCR. The nucleotide sequence was used to express the protein
C in host cells

X Sequence 165 AA;

Query Match 100.0%; Score 846; DB 3; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.3e-86;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 APPRLICDSRVLYRLLLEAKEENITTCGAHCSLNENITVPDKVNFYAWKRMVEVGQA 60

b 1 APPRLICDSRVLYRLLLEAKEENITTCGAHCSLNENITVPDKVNFYAWKRMVEVGQA 60

KW	Chronic renal failure; AIDS; cancer.
XX	
CS	Homo sapiens.
XX	
XX	WO200102017-A2.
XX	
PD	11-JAN-2001.
XX	
XX	28-JUN-2000; 2000WO-EP006009.
PP	
XX	02-JUL-1999; 99US-0142243P.
PR	
XX	05-AUG-1999; 99US-0147452P.
PR	
XX	30-AUG-1999; 99US-0151454P.
XX	
PA	(HOFF) HOFFMANN LA ROCHE & CO AG F.
XX	
PI	Burg J, Hilger B, Josel H;
XX	
DR	WPI; 2001-147051/15.
XX	
PT	Novel erythropoietin-glycoprotein conjugate useful for treating diseases
XX	correlated with anemia in chronic renal failure patients, AIDS and for
PFT	treating cancer, is linked to polyethylene glycol through linker.
XX	
PS	Claim 19; Fig 1; 40pp; English.
XX	
CC	The present invention relates to a conjugate comprising, human
CC	erythropoietin-glycoprotein (EPO) having at least one free amino group
CC	and having in vivo biological activity of causing an increase the
CC	production of reticulocytes and red blood cells, covalently linked to 1-3
CC	lower-alkoxy poly(ethylene glycol) groups through a linker. The invention
CC	is useful for preparation of medicaments for the treatment of prophylaxis
CC	of disease correlated with anemia in chronic renal failure patients
CC	(CRF), AIDS and for the treatment of cancer patients undergoing
CC	chemotherapy
XX	
SQ	Sequence 165 AA;
Query Match 100.0%; Score 846; DB 4; Length 165;	
Best Local Similarity 100.0%; Pred. No. 1.3e-86;	
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 APPRLCDSVLRYLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAWKRMEVGQQA 60
DB	1 APPRLCDSVLRYLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAWKRMEVGQQA 60
QY	61 VEVWQGALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAKAEIS 120
DB	61 VEVWQGALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAKAEIS 120
QY	121 PPDAASAAPLRTTTADTFPKLFrvysnflrgklklytgcactgd 165
DB	121 PPDAASAAPLRTTTADTFPKLFrvysnflrgklklytgcactgd 165
RESULT 8	
AAW53061	
ID	AAW53061 standard; protein; 165 AA.
XX	
AC	AAW53061;
XX	
DT	25-MAR-2002 (first entry)
XX	
DE	Human erythropoietin (hEPO), 165 residue form.
XX	
KW	Human; erythropoietin; EPO; hEPO; haemostatic; red blood cell;
KW	blood disorder; anaemia; chronic renal failure; CRF; AIDS;
KW	acquired immunodeficiency syndrome; cancer chemotherapy; haemostatic;
KW	anti-HIV; antianemic.
XX	
XX	Homo sapiens.
XX	
FH	Key Location/Qualifiers

TT Modified-site 24 /note= "N-glycosylated"

TT Disulfide-bond 29. 33

TT Modified-site 38 /note= "N-glycosylated"

TT Modified-site 83 /note= "N-glycosylated"

TT Modified-site 126 /note= "O-glycosylated"

XX WO200187329-A1.

XX 22-NOV-2001.

XX 08-MAY-2001; 2001WO-EP005187.

XX 15-MAY-2000; 2000EP-00110355.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Papadimitriou A;

XX WPI; 2002-082943/11.

XX Composition useful in the treatment of e.g. AIDS comprises an erythropoietin protein, and a multiple charged inorganic anion in a buffer.

XX Claim 28; Fig 1; 64pp; English.

XX The invention relates to liquid pharmaceutical compositions comprising an erythropoietin (EPO) protein, a multiple negatively charged inorganic anion in a buffer which maintains the pH of the solution from 5.5-7.0, and optionally at least one excipient. The erythropoietin used in the composition is preferably human (AAM53061 or AAM53062) a human erythropoietin variant containing additional glycosylation sites (AAM53064-AAM53107), or an erythropoietin with the C-terminal addition of a C-terminal fragment of human chorionic gonadotropin (AAM53063).

XX Erythropoietin is a glycoprotein essential for the formation of red blood cells and is therefore useful in the treatment of blood disorders characterised by low or defective red blood cell production. The compositions of the invention can be used in the treatment and prevention of anaemia in chronic renal failure patients (CRF), AIDS (acquired immunodeficiency syndrome), and/or for the treatment of cancer patients undergoing chemotherapy. Unlike prior art erythropoietin compositions, the compositions of the invention do not contain human serum albumin (thereby avoiding the possibility of viral infections and allergic reactions associated with this component), are liquid rather than lyophilisates (and therefore do not need to be reconstituted before administration), and are stable at elevated temperatures such as 25 degrees Celsius and even 40 degrees Celsius, and therefore can be stored without refrigeration for prolonged periods without degradation and loss of activity. The present sequence represents the 165 residue form of human erythropoietin which is specifically claimed for use in a composition of the invention

XX Sequence 165 AA;

XX Query Match 100.0%; Score 846; DB 5; Length 165;

XX Best Local Similarity 100.0%; Pred. No. 1.3e-86; Indels 0; Gaps 0;

XX Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLEAKAEENITTCBAEHCNSLNENITVPDTKVNFWAKRMEVQQA 60

Db 1 APPRLICDSRVLYRLLEAKAEENITTCBAEHCNSLNENITVPDTKVNFWAKRMEVQQA 60

QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPPEQLQHVDAVSGLSLTLLRALGAKAEIS 120

Db 61 VEVWQGLALLSEAVLRGQALLVNSQWPPEQLQHVDAVSGLSLTLLRALGAKAEIS 120

QY 121 PDAASAPLRTITADTFKLFVYSNFKLKLKLYTGACRTGD 165

RESULT 9

ABB77896

ID ABB77896 standard; protein; 165 AA.

XX ABB77896;

XX 07-OCT-2002 (first entry)

XX Amino acid sequence of a human erythropoietin (EPO).

XX Human; erythropoietin; EPO; glycoprotein; reticulocyte production; red blood cell production; anaemia; chronic renal failure; acquired immunodeficiency syndrome; AIDS; cancer; bone marrow; committed erythroid progenitor.

XX Homo sapiens.

XX WO200249673-A2.

XX 27-JUN-2002.

XX 08-DEC-2001; 2001WO-EP014434.

XX 20-DEC-2000; 2000EP-00127891.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischler W;

XX Wozny M;

XX WPI; 2002-566640/60.

XX Novel conjugate of erythropoietin glycoprotein with polyethylene glycol, useful for treating diseases correlated with anaemia in chronic renal failure patients and acquired immunodeficiency syndrome.

XX Claim 26; Fig 1; 40pp; English.

XX The present sequence represents a human erythropoietin (EPO) protein. It was used to produce conjugates of the invention. The specification describes a conjugate comprising an EPO glycoprotein having an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its analogues (where hEPO is modified by addition of 1-6 glycosylation sites or a rearrangement of a glycosylation site). The glycoprotein is covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein has in vivo biological activity of causing bone marrow cells to increase production of reticulocytes and red blood cells. The conjugate increased circulating half-life and plasma residence time, decreased clearance, increased clinical activity in vivo, improved potency and stability, when compared to unmodified EPO. The EPO conjugate is useful for preparing medicaments for the treatment and prophylaxis of diseases correlated with anaemia in chronic renal failure patients (CRF), acquired immunodeficiency syndrome (AIDS) and for treating cancer patients undergoing chemotherapy. It is also useful for treating patients by stimulating the division and differentiation of committed erythroid progenitors in the bone marrow

XX Sequence 165 AA;

XX Query Match 100.0%; Score 846; DB 5; Length 165;

XX Best Local Similarity 100.0%; Pred. No. 1.3e-86; Indels 0; Gaps 0;

XX Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLEAKAEENITTCBAEHCNSLNENITVPDTKVNFWAKRMEVQQA 60

Db 1 APPRLICDSRVLYRLLEAKAEENITTCBAEHCNSLNENITVPDTKVNFWAKRMEVQQA 60

QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPPEQLQHVDAVSGLSLTLLRALGAKAEIS 120

Db 61 VEVWQGLALLSEAVLRGQALLVNSQWPPEQLQHVDAVSGLSLTLLRALGAKAEIS 120

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Q: 61 VEVTMOGLIIM SEAVLRGOAL I I VSSOPWEPL OLHVDKAVSGLRSLTLLRALGAQKEAIS 120

b 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHYDKAVSGLSRLTLLRALGAKQEAIS 120
y 121 PPDAASAAPLRITADTFKRLFRVYSNFRGKLYTGACRTGD 165
b 121 PPDAASAAPLRITADTFKRLFRVYSNFRGKLYTGACRTGD 165
RESULT 12
AP70398
D AAP70398 standard; protein; 166 AA.
C AAP70398;
K I 19-FEB-1991 (first entry)
X Sequence of human erythropoietin (EPO).
E Mega-karyocyte-platelet growth factor; hormone;
M mega-karyocyte colony stimulating factor; therapy;
M small acetyl cholinesterase positive cell; erythrocyte growth effect.
K Homo sapiens.
S
X
N JP62149624-A.
X
D 03-JUL-1987.
X
X 15-AUG-1986; 86JP-00191542.
X
X 13-SEP-1985; 85JP-00203049.
X (KAWA/) KAWAKITA M.
X
X WPI; 1987-224837/32.
T Megakaryocyte-platelet growth factor - contains as active component human
T erythropoietin and is used to treat diseases caused by decrease in
T platelets.
S Disclosure; Page 181; 8pp; Japanese.
X
C All of the Cys residues in the SQ are labelled "SH". Megakaryocyte-
C platelet growth factor contains human EPO as an active principle. Human
C EPO has a megakaryocyte colony-stimulating activity and increases the
C ratio of small acetyl cholinesterase positive cell (SachE+) which is
C immature megakaryocyte. Human EPO effects megakaryocyte-platelet system
C other than an erythrocyte growth effect. Megakaryocyte-platelet growth is
C usable as a remedy for diseases caused by a platelet decrease
X
Q Sequence 166 AA;
Query Match 100.0%; Score 846; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.3e-86;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
y 1 APPRLICDSRVLYLLEAKEAENITTCGAHCSSLNENITVPDTKVFYAKRMVEVGQQA 60
b 1 APPRLICDSRVLYLLEAKEAENITTCGAHCSSLNENITVPDTKVFYAKRMVEVGQQA 60
y 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHYDKAVSGLSRLTLLRALGAKQEAIS 120
b 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHYDKAVSGLSRLTLLRALGAKQEAIS 120
y 121 PPDAASAAPLRITADTFKRLFRVYSNFRGKLYTGACRTGD 165
b 121 PPDAASAAPLRITADTFKRLFRVYSNFRGKLYTGACRTGD 165
RESULT 13
AAP70398
D AAP70398 standard; protein; 166 AA.
X

AC AAR23593;
XX 20-OCT-1992 (first entry)
XX Recombinant hematopoietic molecule portion 2.
DE Erythropoietin; EPO: erythrocytes; IL-3; haematopoiesis.
KW
XX Homo sapiens.
OS
XX
PN W09206116-A.
XX
PD 16-APR-1992.
XX
PF 26-SEP-1991; 91WO-US007053.
XX
PR 28-SEP-1990; 90US-00589958.
XX (ORTH) ORTHO PHARM CORP.
XX Rosen JJ;
XX WPI; 1992-150819/18.
DR
XX Recombinant haematopoietic molecules useful in treating anaemia(s) -
PT comprise IL3 or GM-CSF and EPO, G-CSF, IL-5 or M-CSF and has early and
PT later myeloid differentiation activity.
XX
PS Disclosure; Page 32; 82pp; English.
CC This protein sequence given comprises the entire amino acid sequence of
CC human erythropoietin (EPO). EPO leads to the maturation of erythrocytes
CC and is therefore designated as a late myeloid differentiation factor
CC (MDF). Within the scope of the invention hybrid molecules were produced
CC which contain at least a portion of an early MDF and at least a portion
CC of a late MDF covalently linked. The EPO sequence given is effective
CC within the scope of the invention in full or in a truncated version.
CC Amino acids 7-161 act as a late MDF when recombined with an early MDF eg.
CC IL-3. These compounds can be used to promote hematopoiesis in a patient.
CC The bonding of the early and late factors allows a very high conc. of
CC late MDF at the surface of a cell which the early MDF is bound. It also
CC allows the early MDA to act more specifically to stimulate only the
CC desired lineage, thus reducing undesirable effects. These compounds are
CC useful for treating anaemias of various origins eg. renal failure and
CC AIDS. It is easier to produce and administer one recombinant molecule
CC rather than two separate molecules
XX
SQ Sequence 166 AA;
Query Match 100.0%; Score 846; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.3e-86;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 APPRLICDSRVLYLLEAKEAENITTCGAHCSSLNENITVPDTKVFYAKRMVEVGQQA 60
Db 1 APPRLICDSRVLYLLEAKEAENITTCGAHCSSLNENITVPDTKVFYAKRMVEVGQQA 60
Qy 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHYDKAVSGLSRLTLLRALGAKQEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHYDKAVSGLSRLTLLRALGAKQEAIS 120
Qy 121 PPDAASAAPLRITADTFKRLFRVYSNFRGKLYTGACRTGD 165
Db 121 PPDAASAAPLRITADTFKRLFRVYSNFRGKLYTGACRTGD 165
RESULT 14
AAW58404
ID AAW58404 standard; protein; 166 AA.
XX
AC AAW58404;
XX
DT 12-OCT-1998 (first entry)

CC DE Human erythropoietin.
CC AC Erythropoietin receptor agonist; EPO; human; anaemia;
CC XX haematopoietic deficiency; red blood cell; erythroid progenitor;
CC DT bone marrow suppression.
CC DE Homo sapiens.
CC XX WO9818926-A1.
CC XX 07-MAY-1998.
CC XX 23-OCT-1997; 97WO-US018703.
CC XX 25-OCT-1996; 96US-0034044P.
CC XX (SEAR) SEARLE & CO G D.
CC XX McWherter CA, Feng Y, Summers N;
CC XX WPI; 1998-272221/24.
CC XX N-PSDB; AAV31031.
CC XX Human erythropoietin receptor agonist polypeptide - used to stimulate the
CC XX production of red blood cells in a patient.
CC XX Claim 1; Page 93; 112pp; English.
CC XX A claimed human erythropoietin (EPO) receptor agonist polypeptide
CC XX comprises a modified EPO amino acid sequence given in AAW58404, where (a)
CC XX optionally 1-6 amino acids from the N-terminus and 1-5 from the C-
CC XX terminus can be deleted, (b) the N-terminus is joined to the C-terminus
CC XX directly or through a linker (see AAW58405-12) capable of joining the N-
CC XX terminus to the C-terminus, (c) there are new C- and N-termini at any two
CC XX consecutive amino acids from amino acids 23-24 to 38-39, 40-41 to 41-42,
CC XX 43-44 to 48-49, 50-51 to 57-58, 77-78 to 82-83, 84-85 to 88-89, and 108-
CC XX 109 to 131-132, and (d) optionally the agonist polypeptide is preceded by
CC XX Met, Ala, or Met-Ala. 60 Of these circularly permuted EPO receptor
CC XX agonists (see AAW58413-72) are claimed. Also claimed are: nucleic acid
CC XX molecules (see AAV30971-V11030) encoding novel EPO receptor agonists; a
CC XX method of producing an EPO receptor agonist using transformed or
CC XX transfected host cells; and methods for stimulating the production of
CC XX haematopoietic cells, for selective ex vivo expansion of erythroid
CC XX progenitors, and treating patients having a haematopoietic disorder using
CC XX the EPO receptor agonists. The EPO receptor agonists retain one or more
CC XX activities of native EPO and may also show improved haematopoietic cell-
CC XX stimulating activity and/or an improved activity profile which may
CC XX include reduction of undesirable biological activities associated with
CC XX native EPO and/or have improved physical properties such as increased
CC XX solubility, stability and refold efficiency
CC XX Sequence 166 AA;
CC XX Query Match 100.0%; Score 846; DB 2; Length 166;
CC XX Best Local Similarity 100.0%; Pred. No. 1.3e-86;
CC XX Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC XX 1 APPRLICDSRVLYRLLEAKAEANITTCGAHCSLNENITVPDTKVFYAWKMEVGQQA 60
CC XX 1 APPRLICDSRVLYRLLEAKAEANITTCGAHCSLNENITVPDTKVFYAWKMEVGQQA 60
CC XX 61 VEVWQGLALLSEAVLRGQALLVNSQPEPLQHVDAKAVSLRLTLTLRALGAQKEAIS 120
CC XX 61 VEVWQGLALLSEAVLRGQALLVNSQPEPLQHVDAKAVSLRLTLTLRALGAQKEAIS 120
CC XX 121 PPDAAAPLRITTTADTRKLFVRVYSNPLRGLKLYTGEACRTGD 165
CC XX 121 PPDAAAPLRITTTADTRKLFVRVYSNPLRGLKLYTGEACRTGD 165
CC XX RESULT 15
CC XX AAW77780

AAW77780 standard; protein; 166 AA.
AAW77780;
24-NOV-1998 (first entry)
Human EPO receptor agonist polypeptide.
Haematopoietic receptor agonist; erythropoietin receptor agonist; EPO;
human; chimeric protein; stem cell expansion; tumour; infection;
autoimmune disease; haematopoietic disorder; therapy; dendritic cell.
Homo sapiens.
Key Location/Qualifiers
Misc-difference 1..6 /note= "1-6 amino acids of the N-terminus are optionally
deleted"
Misc-difference 23..24 /note= "possible positions of new C- and N-termini"
Misc-difference 24..25 /note= "possible positions of new C- and N-termini"
Misc-difference 25..26 /note= "possible positions of new C- and N-termini"
Misc-difference 26..27 /note= "possible positions of new C- and N-termini"
Misc-difference 27..28 /note= "possible positions of new C- and N-termini"
Misc-difference 28..29 /note= "possible positions of new C- and N-termini"
Misc-difference 29..30 /note= "possible positions of new C- and N-termini"
Misc-difference 30..31 /note= "possible positions of new C- and N-termini"
Misc-difference 31..32 /note= "possible positions of new C- and N-termini"
Misc-difference 32..33 /note= "possible positions of new C- and N-termini"
Misc-difference 33..34 /note= "possible positions of new C- and N-termini"
Misc-difference 34..35 /note= "possible positions of new C- and N-termini"
Misc-difference 35..36 /note= "possible positions of new C- and N-termini"
Misc-difference 36..37 /note= "possible positions of new C- and N-termini"
Misc-difference 37..38 /note= "possible positions of new C- and N-termini"
Misc-difference 38..39 /note= "possible positions of new C- and N-termini"
Misc-difference 39..40 /note= "possible positions of new C- and N-termini"
Misc-difference 40..41 /note= "possible positions of new C- and N-termini"
Misc-difference 41..42 /note= "possible positions of new C- and N-termini"
Misc-difference 42..43 /note= "possible positions of new C- and N-termini"
Misc-difference 43..44 /note= "possible positions of new C- and N-termini"
Misc-difference 44..45 /note= "possible positions of new C- and N-termini"
Misc-difference 45..46 /note= "possible positions of new C- and N-termini"
Misc-difference 46..47 /note= "possible positions of new C- and N-termini"
Misc-difference 47..48 /note= "possible positions of new C- and N-termini"
Misc-difference 48..49 /note= "possible positions of new C- and N-termini"
Misc-difference 49..50 /note= "possible positions of new C- and N-termini"
Misc-difference 50..51 /note= "possible positions of new C- and N-termini"

FT	Misc-difference	127. .128	/note="possible positions of new C- and N-termini"
FT	Misc-difference	128. .129	/note="possible positions of new C- and N-termini"
FT	Misc-difference	129. .130	/note="possible positions of new C- and N-termini"
FT	Misc-difference	130. .131	/note="possible positions of new C- and N-termini"
FT	Misc-difference	131. .132	/note="possible positions of new C- and N-termini"
FT	Misc-difference	162. .166	/note="1-5 amino acids of the C-terminus are optionally deleted"
XX	WO9817810-A2.		
PN	30-APR-1998.		
PD	23-OCT-1997;	97WO-US020037.	
PP	25-OCT-1996;	96US-0029629P.	
PR	(SEAR) SEARLE & CO G D.		
XX	McWherter CA, Feng Y, McKeam JP, Summers NL, Staten NR;		
XX	Streeter PR, Minster NI, Wouffe SL;		
XX	WPI; 1998-261504/23.		
XX	Multi-functional chimeric haematopoietic receptor agonist - useful to		
XX	treat haematopoietic disorders, tumours, infections or autoimmune		
XX	diseases.		
XX	Claim 1; Page 762; 841pp; English.		
XX	A human erythropoietin (EPO) receptor agonist polypeptide comprises a		
XX	modified EPO amino acid sequence of the formula provided in AAW7780, in		
XX	which the N-terminus is joined to the C-terminus directly or via a		
XX	linker, the polypeptide having new C- and N-termini at one of the		
XX	positions indicated. Novel claimed multi-functional chimeric		
XX	haematopoietic receptor agonists (see AAW77812-22) have the formula R1-L1		
XX	-R2, R2-Li-R1, R1-R2 or R2-R1, where L is a linker and R1 and R2 are		
XX	independently selected from: (a) the human EPO receptor agonist; (b) a		
XX	human stem cell factor receptor agonist polypeptide (see AAW77781); (c) a		
XX	human fit-3 receptor agonist polypeptide (see AAW77782); (d) a modified		
XX	human granulocyte colony stimulating factor (G-CSF) polypeptide (see		
XX	AAW77783); (e) modified human interleukin-3 polypeptide (see AAW77784);		
XX	(f) modified human c-mpl ligand polypeptide (see AAW77785); and (g) a		
XX	factor selected from the group consisting of a CSF, a cytokine, a		
XX	lymphokine, an interleukin and a haematopoietic growth factor, provided		
XX	that at least R1 or R2 is selected from (a), (b) or (c) as above. The		
XX	multi-functional chimeric haematopoietic receptor agonist can be used to		
XX	stimulate the production of haematopoietic cells in a patient, for the ex		
XX	vivo expansion of haematopoietic cells, for the production of dendritic		
XX	Query Match	100.0%; Score 846; DB 2; Length 166;	
XX	Best Local Similarity	100.0%; Pred. No. 1.3e-86;	
XX	Matches 165; Conservative	0; Mismatches 0; Indels 0; Gaps 0	
QY	1	APPRICDSRVLYRLYLEAKEAENITTCGAHCSLNEINIVPDTKKNFYAKKMEVGGQA 60	
Db	1	APPRICDSRVLYRLYLEAKEAENITTCGAHCSLNEINIVPDTKKNFYAKKMEVGGQA 60	
QY	61	VEVWGGLLSEAVLRGQALLVNSQWPEQLQHVDAKNSGLRSLLTLRLALGAQKEALS 120	
Db	61	VEVWGGLLSEAVLRGQALLVNSQWPEQLQHVDAKNSGLRSLLTLRLALGAQKEALS 120	
QY	121	PDPAASAPLRITITADTFKRLFRVYSNFLRGKLYTGEACRTGD 165	
Db	121	PDPAASAPLRITITADTFKRLFRVYSNFLRGKLYTGEACRTGD 165	

search completed: May 25, 2004, 11:21:35

Qy	1	APPRLICDSRVLYRLLEAKAEENITTCGAHCSLSNENITVPDTKNFYAWKEMEVGQA	60
Db	1	APPRLICDSRVLYRLLEAKAEENITTCGAHCSLSNENITVPDTKNFYAWKEMEVGQA	60
Qy	61	VEVWGCLALLSEAVLRGQALLVNSQSPWEPLQIHKVDKAVSGLRSLLTTLRALCAQAEIS	120
Db	61	VEVWGCLALLSEAVLRGQALLVNSQSPWEPLQIHKVDKAVSGLRSLLTTLRALCAQAEIS	120
Qy	121	PDDAASAPLRTITADTFRKLFRVYSNFFLRGKLKLYTGEACRTGD	165
Db	121	PDDAASAPLRTITADTFRKLFRVYSNFFLRGKLKLYTGEACRTGD	165

Search completed: May 25, 2004, 11:21:35



QY 121 PPDAASAPLRTITADTFRKLFVYNSFLRGKLYTGCACTGD 165
Db 121 PPDAASAPLRTITADTFRKLFVYNSFLRGKLYTGCACTGD 165

RESULT 7
PCT-US94-04361-37
; Sequence 37, Application PC/TUS9404361
; GENERAL INFORMATION:
; APPLICANT: Brigham and Women's Hospital
; APPLICANT: 75 Francis Street
; APPLICANT: Boston, MA 02115
; APPLICANT: Bunn, H. Franklin
; APPLICANT: Wren, Dany
; APPLICANT: Showers, Mark O.
; TITLE OF INVENTION: Erythropoietin Muteins With Enhanced
; TITLE OF INVENTION: Activity
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04361
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/049,802
; FILING DATE: 21-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0627.336PC01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; PCT-US94-04361-37

Query Match 100.0%; Score 846; DB 5; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.1e-99;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKEANITTCGAECNSLNENITVPDTKKNFYAKRMEVQQA 60
Db 1 APPRLICDSRVLYRLLLEAKEANITTCGAECNSLNENITVPDTKKNFYAKRMEVQQA 60

QY 61 VEVWGGALLSEAVLRQALLVNSSOPWEPLQLHYVDKAVGLRSITLLRALGAKQKAIS 120
Db 61 VEVWGGALLSEAVLRQALLVNSSOPWEPLQLHYVDKAVGLRSITLLRALGAKQKAIS 120

QY 121 PPDAASAPLRTITADTFRKLFVYNSFLRGKLYTGCACTGD 165
Db 121 PPDAASAPLRTITADTFRKLFVYNSFLRGKLYTGCACTGD 165

RESULT 8
US-07-903-220-1
US-07-903-220-1
; Sequence 1, Application US/07903220
; Patent No. 532837

ue May 23 12:51:51 2004

ue 09 030 300 1111

```

; GENERAL INFORMATION:
; APPLICANT: Hewick, Rodney M.
; TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF
; TITLE OF INVENTION: ERYTHROPOIETIN AND ERYTHROPOIETIN COMPOSITION
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Paul H. Heller
; STREET: Kenyon & Kenyon, One Broadway
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/903,220
; FILING DATE: 19920731
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: 1248/27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-1776
; TELEFAX: (202) 429-0796
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-07-903-220-1
; Query Match 100.0%; Score 846; DB 1; Length 193;
; Best Local Similarity 100.0%; Pred. No. 1.4e-99;
; Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 APRRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
; DB 28 APRRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 87
;
; QY 61 VEVWQGLALLSEAVLRQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGQAKAIS 120
; DB 88 VEVWQGLALLSEAVLRQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGQAKAIS 147
;
; QY 121 PPDAASAAPLRITADTFRKLFVYSNFRGLRGKLYTGACRTGD 165
; DB 148 PPDAASAAPLRITADTFRKLFVYSNFRGLRGKLYTGACRTGD 192
;
; RESULT 9
; US-08-883-795A-34
; Sequence 34, Application US/08883795A
; Patent No. 5985607
; GENERAL INFORMATION:
; APPLICANT: Delcove, Genevieve
; APPLICANT: Awang, Gregor
; TITLE OF INVENTION: Recombinant DNA Molecules and Expression
; TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,795A
; FILING DATE: 27-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gravelle, Micheline
; REGISTRATION NUMBER: 40,261
; REFERENCE/DOCKET NUMBER: 7841-062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-883-795A-34
; Query Match 100.0%; Score 846; DB 2; Length 193;
; Best Local Similarity 100.0%; Pred. No. 1.4e-99;
; Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 APRRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
; DB 28 APRRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 87
;
; QY 61 VEVWQGLALLSEAVLRQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGQAKAIS 120
; DB 88 VEVWQGLALLSEAVLRQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGQAKAIS 147
;
; QY 121 PPDAASAAPLRITADTFRKLFVYSNFRGLRGKLYTGACRTGD 165
; DB 148 PPDAASAAPLRITADTFRKLFVYSNFRGLRGKLYTGACRTGD 192
;
; RESULT 10
; US-09-552-265B-4
; Sequence 4, Application US/09552265B
; Patent No. 655343
; GENERAL INFORMATION:
; APPLICANT: Desauvage, Frederick
; APPLICANT: Hennen, Dennis, J.
; TITLE OF INVENTION: NO. 655343el chimpanzee erythropoietin (chepo)
; TITLE OF INVENTION: polypeptides and nucleic acids encoding the same
; FILE REFERENCE: GENENT.057CPl
; CURRENT APPLICATION NUMBER: US/09/552,265B
; CURRENT FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: US 09/307307 ←
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-552-265B-4
; Query Match 100.0%; Score 846; DB 4; Length 193;
; Best Local Similarity 100.0%; Pred. No. 1.4e-99;
; Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 APRRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 60
; DB 28 APRRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKNFYAKRMEVGQQA 87
;
; QY 61 VEVWQGLALLSEAVLRQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGQAKAIS 120

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Db 88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 147
QY 121 PPDAAAPLRTITADTRKLFVYVSNFLRGKLYTGEACRTGD 165
Db 148 PPDAAAPLRTITADTRKLFVYVSNFLRGKLYTGEACRTGD 192

RESULT 11

US-09-554-451-8
; Sequence 8, Application US/09554451
; Patent No. 6680207
; GENERAL INFORMATION:
; APPLICANT: Jonathan Paul MURPHY
; ;
; ;
; TITLE OF INVENTION: Detection of Molecules in Samples
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; ;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; ;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/554,451
; FILING DATE: 15-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/03449
; FILING DATE: No. 6680207ember 16, 1998
; APPLICATION NUMBER: GB 9723955.2
; FILING DATE: No. 6680207ember 14, 1997
; ;
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 165 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ;
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
; ;
; US-09-554-451-8

Query Match 99.6%; Score 843; DB 4; Length 165;
Best Local Similarity 99.4%; Pred. No. 2.6e-99;
Matches 164; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 APRLLICDSRVLYLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAKRMEVQQA 60
Db 1 APRLLICDSRVLYLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAKRMEVQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
QY 121 PPDAAAPLRTITADTRKLFVYVSNFLRGKLYTGEACRTGD 165
Db 121 PPDAAAPLRTITADTRKLFVYVSNFLRGKLYTGEACRTGD 165

RESULT 12

US-09-366-009-34
; Sequence 34, Application US/09366009
; Patent No. 6426042
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; ;
; ;
; Uemori, Takashi
; Koyama, No. 6426042uto
; Hashino, Kimikazu
; ;

; Kato, Ikunoshin
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; CELLS WITH RETROVIRUS
; ;
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; ;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/366,009
; FILING DATE: 02-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,156
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 294382/1995
; FILING DATE: 13-NOV-1995
; APPLICATION NUMBER: JP 051847/1996
; FILING DATE: 08-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 977.6507P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; ;
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 412 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ;
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
; ;
; US-09-366-009-34

Query Match 99.6%; Score 843; DB 4; Length 412;
Best Local Similarity 99.4%; Pred. No. 1.1e-98;
Matches 164; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 APRLLICDSRVLYLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAKRMEVQQA 60
Db 233 APRLLICDSRVLYLLEAKEAENITTCGAHCSLNENITVPDTKVNIFYAKRMEVQQA 292
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
Db 293 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 352
QY 121 PPDAAAPLRTITADTRKLFVYVSNFLRGKLYTGEACRTGD 165
Db 353 PPDAAAPLRTITADTRKLFVYVSNFLRGKLYTGEACRTGD 397

RESULT 13

US-08-809-156B-34
; Sequence 34, Application US/08809156B
; Patent No. 6472204
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; ;
; ;
; Uemori, Takashi
; Koyama, No. 6472204uto
; Hashino, Kimikazu
; Kato, Ikunoshin
; ;
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; ;

TITLE OF INVENTION: CELLS WITH RETROVIRUS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: US/08/809,156B
FILING DATE: 07-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PCT/JP96/03254
FILING DATE: 07-NOV-1996
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION DATA:
JP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977,6507P
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-809-156B-34

Query Match 99.6%; Score 843; DB 4; Length 412;
Best Local Similarity 99.4%; Pred. No. 1.1e-98;
Matches 164; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLICDSRVLYRLLLEAEENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 60
DB 233 APPRLICDSRVLYRLLLEAEENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 292
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVDAVSGRLSLTTLRALGAKKEAIS 120
DB 293 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVDAVSGRLSLTTLRALGAKKEAIS 352
QY 121 PPDASAAPLRTITADTFKRLFRVYSNFRGLRGKLYTGEACRTGD 165
DB 353 PPDASAAPLRTITADTFKRLFRVYSNFRGLRGKLYTGEACRTGD 397

RESULT 14
US-09-552-265B-2
Sequence 2, Application US/09552265B
Patent No. 6555343
GENERAL INFORMATION:
APPLICANT: Desauvage, Frederick
APPLICANT: Henner, Dennis, J.
TITLE OF INVENTION: No. 6555343el chimpanzee erythropoietin (chepo)
TITLE OF INVENTION: polypeptides and nucleic acids encoding the same
FILE REFERENCE: GENENT.057CPI
CURRENT APPLICATION NUMBER: US/09/552,265B
CURRENT FILING DATE: 2000-04-19
PRIOR APPLICATION NUMBER: US 09/307307

PRIOR FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 193
TYPE: PRT
ORGANISM: Pan troglodytes
US-09-552-265B-2
Query Match 99.1%; Score 838; DB 4; Length 193;
Best Local Similarity 99.4%; Pred. No. 1.4e-98;
Matches 164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 APPRLICDSRVLYRLLLEAEENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 60
DB 28 APPRLICDSRVLYRLLLEAEENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVDAVSGRLSLTTLRALGAKKEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVDAVSGRLSLTTLRALGAKKEAIS 147
QY 121 PPDASAAPLRTITADTFKRLFRVYSNFRGLRGKLYTGEACRTGD 165
DB 148 PPDASAAPLRTITADTFKRLFRVYSNFRGLRGKLYTGEACRTGD 192

RESULT 15
US-09-552-265B-5
Sequence 5, Application US/09552265B
Patent No. 6555343
GENERAL INFORMATION:
APPLICANT: Desauvage, Frederick
APPLICANT: Henner, Dennis, J.
TITLE OF INVENTION: No. 6555343el chimpanzee erythropoietin (chepo)
TITLE OF INVENTION: polypeptides and nucleic acids encoding the same
FILE REFERENCE: GENENT.057CPI
CURRENT APPLICATION NUMBER: US/09/552,265B
CURRENT FILING DATE: 2000-04-19
PRIOR APPLICATION NUMBER: US 09/307307
PRIOR FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 193
TYPE: PRT
ORGANISM: Pan troglodytes
US-09-552-265B-5

Query Match 98.6%; Score 834; DB 4; Length 193;
Best Local Similarity 98.8%; Pred. No. 4.6e-98;
Matches 163; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 APPRLICDSRVLYRLLLEAEENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 60
DB 28 APPRLICDSRVLYRLLLEAEENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVDAVSGRLSLTTLRALGAKKEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVDAVSGRLSLTTLRALGAKKEAIS 147
QY 121 PPDASAAPLRTITADTFKRLFRVYSNFRGLRGKLYTGEACRTGD 165
DB 148 PPDASAAPLRTITADTFKRLFRVYSNFRGLRGKLYTGEACRTGD 192

Search completed: May 25, 2004, 11:24:06
Job time : 24 secs